

N:Alternate names: protein B2A19.180
 C:Species: Neurospora crassa
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 24-May-2001
 C:Accession: T51084
 R:Schulte, U.; Allyn, V.; Hehse, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000
 A:Reference number: 225286
 A:Accession: T51084
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1,297 <SCH>
 A:Cross-references: EMBL:AL390092, GSPDB:GN00116, NCSP:B2A19.180
 A:Experimental source: BAC clone B2A19, strain OR744
 C:Genetics:
 A:Gene: NCSP:B2A19.180
 A:Map position: 6
 A:introns: 218/1; 249/1
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.6%; Score 335.5; DB 2; Length 297;
 Best Local Similarity 31.7%; Pred. No. 4.8e-19;
 Matches 97; Conservative 39; Mismatches 103; Indels 67; Gaps 8;

QY 6 RSVKGLAVITGGAGSGGLATAEPLVGGASAVLLDLPNS-----GGBAQ 50
 DB 2 RSLHKAQLITGGSGGSLATARHLYEGCVTLTIGRESTLRQASQSLLSQPLHSPAQ 61
 QY 51 AKKLGNNCFAPADVTSEKDVOTAL-ALAKKFGHVDVAVNCAGIAVAS---KTYNLEKG 106
 DB 62 QPSDTKRVSYHPLNNTASSWEDLLQSNKSGKGRVVDLLNCAGITGRPLMKT----- 115
 QY 107 QHTLEDSQRYLDVLMGTFVIRLVAGEMQONEP-----DOG- 145
 DB 116 ---SLEEVGLLDITLRLRTVYLCKFKYGRAMLRNRSSQGHPRKADGGAEGWSTEEEG 172
 QY 146 -----ORGVIIINTASYAAFEQGVGAAYASASGSGIVGKTLPLARDLAPIGI 191
 DB 173 KGEKGQGVREGVQERGVYIINVASLQKGYIGTSVYAAAKGVGLTSLAHEYGRSGI 232
 QY 192 RYMTAPGLFEGPLTSLPEKVCNFIASOVPPSRGLGPAPAEYAHLYQAIIENPFLNGEVI 251
 DB 233 RYNAVLPGYIEIDMTTGLKNP---SILQOIFL-GFGTITDEVADAALPLIKNPYANNCVL 288
 QY 252 RLDGAI 257
 DB 289 NLDGGL 294

RESULT 14
 AS0042
 3-Oxocetyl-[acyl-carrier protein] reductase [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AH2042
 R:Kaneko, T.; Nakamura, Y.; Molk, C. P.; Kurita, T.; Sasamoto, S.; Watanabe, A.; Iriguich, Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 6, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
 A:Reference number: AB1807; M0ID:21595285; PMID:11759840
 A:Accession: AH2042
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-251 <KUR>
 A:Cross-references: GB:BA000019, PIDN:BA075593.1, PID:q17130984, GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: fabG
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.6%; Score 334.5; DB 2; Length 251;
 Best Local Similarity 33.1%; Pred. No. 4.6e-19;
 Matches 97; Conservative 46; Mismatches 97; Indels 41; Gaps 7;

0Y 1 MAAACRSVKGLVAVITTGAGAGLGIATNERLVGGAGASA-----VLLDLEPNSGG 47

Db 1 MALISENLRQGVAVVITGASRGIGRAIMALELANGATVAVVYKASSSTAADAEVAEITGAG 60

0Y 48 EAQAKRTGNNCVAPADAVTSEKDYQPTLALAKGKFGVNDVAVACAGAAVASKTYNLNKKQ 107

Db 61 EAVALK-----ADVSOVEVDNLINGAIDCFKRIDVLVNNAGTTRDTLLRKRP--- 109

0Y 108 THLEEDPQRYLDVNLMTGFNNVIRLVAGEMGONEPDGGQRGVITINTASVAFEGVYQGA 167

Db 110 ----EDMGAVIDLNLGVFLCTRAVSKLMKKO-----RSGRIINTITSVAGOMGNQGAN 159

0Y 168 YSASKGGLVGTPLPIADLPAGIGRVNTIAPGLFGFTPLSLDEKYNFLASQVPPPSRL 227

Db 160 YSAAKAVYIGFTKIVAREELISRGITVANAVAPGTATMTISLAKSE---GILQYIPL-GRY 215

0Y 228 GDPAEYALHVAQIENP---FLNGEVIRLDGAIRM 259

Db 216 GQPEELINGMVRFLADPAAPAVITTGQVENVNGMVM 250

RESULT 15

S22450

3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) precursor, NADPH-dependent

N:Alternate names: beta-ketoacyl-ACP reductase

C:Species: Cuphea lanceolata

C:Date: 16-Feb-1995 #sequence_revision 23-Feb-1996 #text_change 17-Mar-2000

C:Accession: S22450; S19632

R:Klein, B.; Pawlowski, K.; Hoerlcke-Grandpierre, C.; Schnell, J.; Toepfer, R.

Mol. Gen. Genet. 233, 122-128, 1992

A:Title: Isolation and characterization of a cDNA from Cuphea lanceolata encoding a b

A:Reference number: S22450; MUID:92293104; PMID:1376402

A:Accession: S22450

A:Molecule type: mRNA

A:Residues: 1-320 <KLP>

A:Cross-references: EMBL:X64566; NID:g18045; PIDN:CAA5866.1; PID:g18046

A:Experimental source: Immature embryo

C:Genetics:

A:Gene: Ckr27

A:Genome: nuclear

C:Function:

A:Description: EC 1.1.1.100 [validated, MUID:92293104]

A:Pathway: fatty acid biosynthesis

A>Note: Integral part of the fatty acid synthase type II

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C:Keywords: chloroplast; fatty acid biosynthesis; NADP; oxidoreductase

F:1-63/Domain: transit peptide (chloroplast) #status predicted <TNP>

F:64-320/Product: 3-oxoacyl-[acyl-carrier-protein] reductase #status predicted <MAT>

F:78-258/Domain: short-chain alcohol dehydrogenase homology <SADH>

F:227/Active site: Tyr #status predicted

Query Match 25.5%; Score 334; DB 2; Length 320;

Best Local Similarity 32.7%; Pred. No. 6.8e-19;

Matches 87; Conservative 46; Mismatches 11; Indels 22; Gaps 6;

0Y 2 AAGCSRSKGLVAVITGAGAGLGIATNERLVGGAGASAVLLDLEPNSGGA-----QAQKIGN 56

Db 69 AAGGSGVSPVYIVTGASRGIGKATALSL-GRAGKGLVLYNARSSKEADEVSKIEIARGG 127

0Y 57 NCVEAPADVTSEKDYQPTLALAKGKFGVNDVAVACAGIAVASKTYNLNKKQTHTEDEQR 116

Db 128 QALTEGDDSKEDVEAMKTAVDAMGVTDLVNNAGTTRDGLIMRKRSQ-----WQE 181

0Y 117 VALDVNLMTGFNNVIRLVAGEMGONEPDGGQRGVITINTASVAFEGVYQGA 176

Db 182 VIDNLNLTGFLCTQAAKIMKK-----KKRIINIASVGLVGNAGAGNSAAKAGVI 235

0Y 177 GMTLPIARDLAPIGRVNTIAPGLFGFTPLSLPERKYNFLASQVPPPSRLGDPAEYALH 236

Db 236 GFTKTVAREYASRNNVNNVAPAGFTISSDMTSLKGLDINKKILLETIPL-GRYGGQPEEVAGL 294

237 YQAATFNP---FLNGEVIRLDGAIRM 259

RESULT 10
 F83098
 Probable short-chain dehydrogenase PA4389 [imported] - *Pseudomonas aeruginosa* (strain PA
 C:Species: *Pseudomonas aeruginosa*
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: F83098
 C:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
 A:Reference number: A82950, MUID:20437337, PMID:10584043
 A:Accession: F83098
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-252 <STO>
 A:Cross-references: GB:AE004854; GB:AE004091; NID:9950606; PIDN:AG07777.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA4389
 A:Superfamily: rhlB101 dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 27.1%; Score 355; DB 2; Length 252;
Best Local Similarity 35.1%; Pred. No. 1.1e-20;
Matches 94; Conservative 40; Mismatches 100; Indels 34; Gaps 7;

```

OY      8 VKGLAVITGASGLGATAEELVYGQASAVLLDLPN-----SGGEQAKRLG 55
DB      3 LKDVYIIITGGCGIGRAMEYLAGKGRALVLDINERLDEAVAACKAGGDRA---- 58
OY      56 NNCFAPADVYSEKDVOTALALAKGFRVDVANCAGIAVASKTYLKKQOTH--TLED 113
DB      59 -----LYCQNAVDEQVETMVAQVASFAGINGLVNNAGIILDGLTIKVKDQGLSKMSIAQ 113
OY      114 FQRLVDVLMKTFNVIRLVACEMGQ--NEPQGGQGRGVIITNTASVAEFGQGVGAASAS 171
DB      114 WQSIDVNLTVFICTREVAAKMTELKNE-----GALVVISSTISR-AGMAGQANTSA 165
OY      172 KGIIVGMLPTARDIAPGIRGIMTIAPLFGTPLITSLPKVCNFEASQVFPSPRLGPPA 231
DB      166 KAGVADADVVAKEELARIGIRVAGAPGFISTEMTAGKPEALEKMTAGIPL-RKMGKPV 224
OY      232 EYAHLYOAIENPFLENGVIRLDGAIRM 259
DB      225 EIAHSVAIFENDYYTGRVLELDGRL 252

RESULT 11
F97338
3-ketoadyl-acyl carrier protein reductase [imported] - Clostridium acetobutylicum
C.Species: Clostridium acetobutylicum
C.Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C.Accession: F97338
R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Marfakova, K.S.; Zeng, Q.; Gibson, R.; Lee
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4833-4838, 2001
A.Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A.Reference number: A96900; MUID: 21359325; PMID: 21359325
A.Accession: F97338
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-249 <KUR>
A.Cross-references: GB:AE001437; PIDN:NAK81497.1; PID:q15026670; GSPDB:GN00168
A.Experimental source: Clostridium acetobutylicum ATCC824
C.Genetics:
A.Sequence: CAC3574
C.Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
```

```

QY      VKELVAVITGGASGJLALAEALVQGASAVILLEDPNGGGAQ-----AKKGNVCYAP 62
Dd      5 LSKKAVAVTGAGRGRLRALALAKLAAGNIV- VNRSEAEATQALKEIBELSGKAAYK 63

QY      63 ADVTSEKDVOYALALAKGKRGVDVAVNCAGIYASKTYLNKKQTHLEDPOYEDVNL 122
Dd      64 ADISKDEDEETIIKKALDEYGVTDILVNNAGITKDNLLRPKE-----EDFOSVIVNL 117

QY      123 MGFENVIRLAVGMEGNEDDGGGSGVITNTASVAFAEGVQGOAAYSASKGGIYGMTLP1 182
Dd      118 KGAFNCRICKHTRSRMLK-----KSGKIINISVGLIGLGNAGOVNYYAARAGIIGMKSV 171

QY      183 ARDLAPLIGIRVMTIAGLGTGTPLLTSLPEKYCNFLASOVPPPSRLGDPAEYAHLVQAIIE 242
Dd      172 AKELASGITVNAVAAGIISKDMTALTDKQRESIYAAPL- NRVGEAEADVANLVLEFLAS 230

QY      243 --NPPLNGEYVIRLDSAIRM 259
Dd      231 DLSYITIGOVINVDGGMV 249

```

RESULT 12

H72219
C:oxoacyl-(acyl carrier protein) reductase - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: H72219
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Har-
rington, J.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
M.C.

Nature 399, 323-329, 1999
A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A12200; MID:99287316; PMID:10360571
A:Accession: H72219
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-246 <ARN>
A:Cross-references: GB:A5001811; GB:A5000512; NID:g4982291; PIDN:AAD36790.1; PID:g498
A:Experimental source: strain MSB8
C:Genetics:
G:Gene: TM1724
G:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology <SAB>
F:6-185/Domain: short-chain alcohol dehydrogenase homology <SAB>

Query Match 26.1%; Score 341; DB 2; Length 246;
Best Local Similarity 33.7%; Pred. No. 14e-19;
Matches 86; Conservative 47; Mismatches 104; Indels 18; Gaps 5;

DY 8 VKGLVAVITGGASGIGLATAEELVGQGSANVLDDLPNSGEH---QAKKLGNNCVTFAPAD 64
 :::|||:|||::||| :::|||:: :
DB 3 LEGRKCLLTGTGASGSGKATTLTFAOEGATTAGISIKENIDLWKEAGLPGKYDPAVLN 62
 :||:|||||||::| :||:|||||||::| :
DY 65 VTSEKDVOFTALALAKGKRVDVANVCAGIAYASKTYLNLRKGTHTEDEDFORYLDVMDMG 124
 ||:|||:|||||||::| :||:|||||||::| :
DB 63 VTDHQIQIEVEYERVKQGKRGIDLVNNNGITIRDALIVMKRE-----EDMDAVINVLKMG 116
 :||:|||||||::| :||:|||||||::| :
DY 125 TENVTRLVAGEKQNEPDQGGORGYIINTASVAAFEGGVCGAAASASXSGGIYGVTLPILAR 184
 |||::|:|||||||::| :||:|||||||::| :
DB 117 VFNVQMWVPYMIKQ-----RNGSLTVSSSVGIYGNPQTNAASAAGVIGMTKWAK 170
 :||:|||||||::| :||:|||||||::| :
DY 185 DLAPIRKMTIAPIPLFGTIPLTSPKEVCAKFLLASOVPEPSRLGDPPAAPHLV--QAITE 242
 |||||:|||||||::| :||:|||||||::| :
DB 171 ELAIGINVNNAVAPFIETPTERTKLEPKARRTALSRIPL-GRFGKPEVACVIIFLASDE 229
 :||:|||||||::| :||:|||||||::| :
DY 243 NFPLNGEYTRLDGA I 257
 ::||:|||||||::| :||:|||||||::| :

DB 230 SSYTVGVGVIGDIGDL 244

RESULT 13
T51084
3-oxoacyl-[acyl-carrier-protein]-reductase (oar-1) [Imported] - *Neurospora crassa*

RESULT 7

Ag2750
3-hydroxyacyl-CoA dehydrogenase type II Atu1415 [imported] - Agrobacterium tumefaciens C3Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence.revision 11-Jan-2002 #text.change 01-Feb-2002
C/Accession: AG2750
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, I.; Kap, P.; Gillet, W.; Grant, C.; Guentherer, D.; Kutayvin, T.; Levy, R.; Li, M.; McCellerage, G.; Miller, W.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.

A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AG2750
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-257 <KUD>
A:Cross-references: GB:AE006688; PIDN:AAL42421.1; PID:g17739833; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu1415
A:Map position: circular chromosome
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 49.0%; Score 642; DB 2; Length 257;
Best Local Similarity 51.7%; Pred. No. 3.le-43;
Matches 134; Conservative 41; Mismatches 76; Indels 8; Gaps 3;

DQ 7 SVKGLVAITGSGSLGATTAERLVGGASAVLDLPNSGGEAQKRLGNCCVFAPADVT 66
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2 NIEGAGAVTGAOSLGAAVARMALARCAATYIFRNEDACKKLAAELGKAV--QGCVT 59
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 67 SEKDVTALALAKGFGVDVAVNCAGIAYASKITYNLKKQTHTLEDQRVLVDNLMTGF 126
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 SDAPAQAALKVAAASAKGSLRLVWCAGIGTAGRI--LGRSGPQLGDDEQVIRVNLIGTF 117
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 127 NVIRLVAGEMGONFERDQG----GGRGVIIINTASVAFAFGOVGOAAYSAKSGIVGMTLPI 182
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 118 NMRLAAAHMAEREDEDQSDSRONGVIYVNASVAFAFGQIGQAAAYSAKSGIVSLALPA 177
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 183 ARDLAPGIRWTTIPGFLPTLSPEKYCNPLASQVPPSSRLGDPDAEYHLYQALIE 242
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 178 ARELARFRIRNTVAPGILFPLPGGLPEVOESLAGGIIPHSRLGDPDAEFADVIRFLIE 237
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

DQ 243 NPFLNGEVIRLDGAIRMOP 261
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 238 NDYNGEVIRLDGAIRMOP 256
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8

C87264
3-hydroxyacyl-CoA dehydrogenase [imported] - Caulobacter crescentus C3Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence.revision 20-Apr-2001 #text.change 10-May-2001
C/Accession: C87264
R:Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A>Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: AB7249; MUID:21173698; PMID:11259647
A:Accession: C87264
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-260 <STO>
A:Cross-references: GB:AE005673; NID:g13421233; PIDN:AAK22111.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC0124
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

	Query Match	45.5%; Score 595; DB 2; Length 260;	
	Best Local Similarity	51.0%; Pred. No. 1,6e-39;	
	Matches 130; Conservative	30; Mismatches 89; Indels 6; Gaps 2;	
QY	11 LVAVITGGAGGLGATATRLVVGOGASAVLLDPLRNSGGEAOKKLGNNCPADPVSSEKD	70	
Dd	: : : : : : : : : :		
Dd	7 VAAVTGGAGGLDEPRARALAAQGVKALFDNMEERGLQAYKEIG--VFCKNVISDDAD	64	
QY	71 VCFALALAKRFGRVDVAVNCAGIAVASKTYNLRKGQTHP----LEDFOVLVDNLNGTF	126	
Dd	: : : : : : : : : :		
Dd	65 VDAAFEKRAAHAGGERILTVACAGTGNNAKAFASDKATGETKHPELDLFRDIIOINLVGF	124	
QY	127 NVFLVASEGONPPDOGGORGVITNTASVAEEGGVOGAAYSASKGIVGMTLPARDL	186	
Dd	: : : : : : : : : :		
Dd	125 RCIARKSKMLDDELDEGERALVNASVAEEDQGCAIYASKSQGVGMILLPIARDL	184	
QY	187 APIGIRVMYTIAPGLFTGPLLTSLPEKYCNFLASOVPEPSRLGDPAEYAHVQAIIENPL	246	
Dd	: : : : : : : : : :		
Dd	185 MGSEIRVNTILPGIFNPPLMNNAPFAVKAGLAASVPFPPKRGHPEFYAQIALTIMTCGYF	244	
QY	247 NGEVIRLDGAIIRMOP 261		
Dd	: : : : : : : : : :		
Dd	245 NGEDVRIDGGIRMAP 259		
	RESULT 9		
E70740	probable fabG2 protein - Mycobacterium tuberculosis (strain H37RV)		
C:Species:	Mycobacterium tuberculosis		
C:Dere:	17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000		
C:Accession:	E70740		
R:Coile, S.I.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon			
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtzoyd,			
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.			
Nature 393, 537-544, 1998			
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.			
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno-			
A:RefSeq number: A70500; MUID:98295987; PMID:9634230			
A:Accession: E70740			
A>Status: preliminary; nucleic acid sequence not shown; translation not shown			
A:Molecule type: DNA			
A:Residues: 1-247 <COL>			
A:Cross-references: GB:275555; GB:AL123456; NID:g3261608; PIDN:CAA99983.1; PID:g14190			
A:Experimental source: Strain H37RV			
C:Genetics:			
A:Gene: fabG2			
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology			
F:8-186/Domain: short-chain alcohol dehydrogenase homology <SAND>			
Query Match	29.3%; Score 383.5; DB 2; Length 247;		
Best Local Similarity	38.9%; Pred. No. 6.4e-23;		
Matches 96; Conservative	43; Mismatches 91; Indels 17; Gaps 5;		
QY	13 AVITGASGLIATAERLYVGOGASAVLLDPLNSGGEAOKKLGNN--CVFAPADVSEKD	70	
Dd	: : : : : : : : : :		
Dd	10 AVITGGAGGLGATATRLVVGOGASAVLLDPLNEATEVAKKLGGDDVALAVRCVTDQDD	69	
QY	71 VQTALALAKGFGRRDVAVNCAGIAVASKTYNLRKGQTHLEDPQRVLVDNLMTFNVR	130	
Dd	: : : : : : : : : :		
Dd	70 VDLIRLRAVERFFGGIDVVANNAGSTRDPTM-----RTMETEQPDQYIAHLKFTWNGTR	123	
QY	131 LVAGEMGONPPDOGGORGVITNTASVAEEGGVOGAAYSASKGIVGMTLPARDLPIG	190	
Dd	: : : : : : : : : :		
Dd	124 LAAATMPRR-----KRDAIYMSSVSGKVGWGCTNYSAAKAGIVGTAKAAKELALTG	177	
QY	191 IRYMTIAGLTGTPLTLTSLPEKYCNFLASOVPEPSRLGDPAEYAHVQAIIIE--NPFLG	248	
Dd	: : : : : : : : : :		
Dd	178 IRVNAIAGGLIRSAMTEAMPORINDQILAEPV--GRAGESEVASVAFTLASDSLSTYTG	236	
QY	249 EVIRLDG 255		
Dd	: : : : : : : : : :		
Dd	237 TVLDVTG 243		

Probable dehydrogenase - Mycobacterium tuberculosis (strain H37RV)
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #ext_change 20-Jun-2000
C/Accession: A70534
R/Cole, S.T.; Brosch, R.; Parthill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
R/Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
R/Janstead, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98255987; PMID:9634230
A/Accession: A70534
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-250 <COL>
A/Cross-references: GB:J95584; GB:AL123456; NID:g3261774; PID:CA809032.1; PID:g2117182
A/Experimental source: strain H37RV
C/Genetics: RV1144
A/Gene: RV1144
C/Family: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology <SAB>
C/Domain: short-chain alcohol dehydrogenase homology <SAB>
Query Match 51.3% Score 671.5; DB 2: Length 250;
Best Local Similarity 60.1%; Pred. No. 1.4e-45;
Matches 152; Conservative 25; Mismatches 69; Indels 7; Gaps 4;
OY 9 KGLVAVITGGASGLTARLVGCGASAVLDDLPNSGCGAOKKLGNNVCFAPADYTS 68
DB 4 KDAVAAYVTGGASGLTARLVGCGASAVLDDLPNSGCGAOKKLGNNVCFAPADYTS 60
OY 69 KDVOFATLAKGKRGPDVAVNCAGIYVASKRTNLKKGQHTLEDYFQVLDVLMGTFNY 128
DB 61 AAVSNALIELA-DSLGPYRVVYVNCAGTGNALRV--LSMDGVFPLAFAFKIYDNLVGFENV 117
OY 129 IRLVAGMGONPEPQGGQGVYITNTASVAAPFEGVCGAASASAKGIGVGTLPDARDLAP 188
DB 118 IRLAERIAKTEP-IGEEGVYITNTASVAAPFEGVCGAASASAKGIGVGTLPDARDLAP 176
OY 189 IGIVWMTIAPGLFTPLTSLPEKVCNPLASQVPEPFRSLDPPAEYAHVQALLENPFLNG 248
DB 177 KLIVVITAPGLFTPLTSLPEKVCNPLASQVPEPFRSLDPPAEYAHVQALLENPFLNG 236
OY 249 EVIRLDGAIKMP 261
DB 237 EVIRLDGAIKMP 249
RESULT 5
H95360
Probable [Imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSYMA
C/Species: Sinorhizobium meliloti
C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #ext_change 30-Sep-2001
C/Accession: H95360
R/Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
R/Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A/Title: Nucleotide sequence and predicted functions of the entire sinorhizobium meliloti
A/Reference number: A95262; MUID:21396509; PMID:11481432
A/Accession: H95360
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-355 <KUN>
A/Cross-references: GB:AB06469; PID:AAK65450.1; PID:g14523918; GSPDB:GN00165
A/Experimental source: strain 1021, megaplasmid pSYMA
R/Gilbert, F.; Finan, T.M.; Long, S.R.; Punler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chait, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Leilaure,
Hubert, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A/Title: The complete genome of the legume symbiont Sinorhizobium meliloti.
A/Reference number: A96039; MUID:21368234; PMID:11474104

C:Genetics:
A:Gene: SmaI452
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 51.2%; Score 670; DB 2; Length 255;
Best Local Similarity 54.7%; Pred. No. 1,9e-45;
Matches 139; Conservative 34; Mismatches 79; Indels 2; Gaps 1;

OY 8 VKGLVAVITGASGLATAEERLVGGQASAVLLDLPNSGGEQAOKKLGNCCVPADYTS 67
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 3 LKSRVFYVTGSSSLGAAYTRMLAQEGATVGLDLKPRAEEPAELGAAYRRNMDYIN 62
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
OY 68 EKDVQTALALAKGFGRVDVAVNCAGTAAVSATYNLKKGTHTLEDFORVLNVNMGTEN 127
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 63 EADATTAALAFKAQEFHGHVHLVNCAGTAPBEKI - LGRSGPHALDSFARTVAVNLTGEN 120
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
OY 128 VIRIVAGEMGNPEPDGOGGVITNTFAVSAAFEGOVGOAAYSASKGIYGMTPIARDLA 187
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 121 MIRLAELVMSGSEFDADAGERCVLYNTASIAFPDQIQGMAYNAASKGVVALTLPPARELA 180
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
OY 188 PIGIRVMTIAPGLFTPLTSLSPKVONFLASOYPPPSRLGDPAEVAHLVQALITENFNL 247
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 181 REGIRVVYTIAPGITDETPMMAGMPDODDALAASVFPFPRRLGRAEYVAALVKHICENTMLN 240
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
OY 248 GEVIRLDGARIMOP 261
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 241 GEVIRLDGALRMAP 254
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

RESULT 6
P97531
Probable short-chain dehydrogenase (PA2554) [imported] - Agrobacterium tumefaciens (S)
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirolo, B.; Goldm
A.: Liu, F.; Wollam, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2333-2328, 2001
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A:Reference number: A97359; PMID:11743194
A:Accession: F97531
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-257 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAR87207.1; PID:g15156487; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C2613
A:Map position: circular chromosome
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 49.0%; Score 642; DB 2; Length 257;
Best Local Similarity 51.7%; Pred. No. 3.1e-43;
Matches 134; Conservative 41; Mismatches 76; Indels 8; Gaps 3;

OY 7 SVKGVAVITGASGLATAEERLVGGQASAVLLDLPNSGGEQAOKKLGNCCVPADYT 66
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 2 NIEGAGALVTGAASGLGAAYARMKLARGAAVTIPDRNEGACKLILAEIGKAV--QGDT 59
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
OY 67 SEKDVTALALAKGFGRVDVAVNCAGTAAVSATYNLKKGTHTLEDFORVLNVNMGTF 126
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 60 SDADAQAALIKVAASAKSGGIRLILVNCAGTIGTGRI - LGREGQPQLGDEQVIRVNLDTF 117
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
OY 127 NVIRLVAGEMGNPEPDG---GGRGVINTASVAAFEGOVGOAAYSASKGIYGMTLPI 182
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 118 NMRLAAAHMAHEREDGEDGDSRDNGVIYNTASVAAFEGQIGOAAYNAASKGIYSALPA 177
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
OY 183 ADLAPIGIRVMTIAPGLFTPLTSLSPKVONFLASOYPPPSRLGDPAEVAHLVQALITE 242
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 178 ARELARFRIRVMTVAPGLFTPLDGLDQEVOESLIAGIIPPSRLGDPAEVAHDYVRLTE 237
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
OY 243 NEPLNGEVIRLDGARIMOP 261
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

ALIGNMENTS

RESULT 1
T20484
hypothetical protein F01G4.2 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C:Accession: T20484
R.Harris, B.
submitted to the EMBL Data Library, January 1996
A:Reference number: 219281
A:Accession: T20484
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-258 <M1>
A:Cross-references: EMBL:268341; PIDN:CAA92764.1; GSPDB:GN00022; CESP:F01G4.2
A:Experimental source: Clone F01G4
C:Genetics:
A:Gene: CESP:F01G4.2
A:Map position: 4
A:Intons: 8/3; 116/3; 162/3; 209/3
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match

57.1%; Score 748; DB 2; Length 258;
Best Local Similarity 59.9%; Pred. No. 1.4e-51;
Matches 154; Conservative 34; Mismatches 67; Indels 2; Gaps 1;

QY 3 AACRSYKGLVAVITGGASGLGATAEERLYVGOGASAVLDDLPNSGGEAQAOKKLGNNCVAPADYTS 62
DB 2 SALRSKRGVALVTGGASGLGKAALFVLAQAQVAIIDLPQSKADYAKETGG--ITFP 59
QY 63 ADVTSEKDVQALALAKGKFGNVDAVNCAGIAVASKTYNKKGGTHTLEDFQRYLVNVL 122
DB 60 ASVTSEEEVRAFAKVAQAEYGRDLVNCAGIAVAFKYSVQKKHVDPEKIRQTIIDVNV 119
QY 123 MGFENYRLVAGMGQNEPDGQGRVITNTASVAEFEGOVQAAYASAKSGIVMTLPI 182
DB 120 LGFENYIRGVALMGHEKNDANGQKRVINTASVAFFDQGTQGSASKGAIVGMTLPI 179
QY 183 ARDLAETGRVMTIAPGLTGTPLTSLPEKVCNFTLASQVPPPSRLGDPAEYAHVQAITE 242
DB 180 ARFPADGIRFNTIAPGLTGTPLTSLPEKVSFLAQLIPNSRLGHPHEYALVQHILE 239
QY 243 NPFLNGEVIRLDGAI RM 259
DB 240 NQYLNGEITRFDGAL RM 256

RESULT 2
H83326
probable short-chain dehydrogenase PA2554 [imported] - *Pseudomonas aeruginosa* (strain PA
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H83326
R.Stover, C.K.; Pham, X.Q.; Ewlin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Bz
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, J.; Linn,
J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A:Reference number: A82950; M01D:20437337; PMID:10984043
A:Accession: H83326
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-255 <STO>
A:Cross-references: GB:AE004683; GB:AE004091; NID:g9948607; PIDN:AAG05942.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2554
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 55.0%; Score 720; DB 2; Length 255;
Best Local Similarity 57.5%; Pred. No. 2.3e-49;

Matches 145; Conservative 39; Mismatches 66; Indels 2; Gaps 1;
QY 8 VKGLVAVITGGASGLGATAEERLYVGOGASAVLDDLPNSGGEAQAOKKLGNNCVAPADYTS 67
DB 3 IENRVFLITGGASGLGAASVAKAVLLDVNAEAGAKALGASARFQRTYAS 62
QY 68 EKDVTALALAKGKFGNVDAVNCAGIAVASKTYNKKGGTHTLEDFQRYLVNVL 127
DB 63 EADGRQAVAAALAEAFGLHGLACAGVAPAEKY--LGRNIGHALSESFRVIDINLVGSPN 120
QY 128 VIRLVAGMGQNEPDGQGRVITNTASVAEFEGOVQAAYASAKSGIVMTLPIARDLA 187
DB 121 MLRLAAEAMSGQPDGEGRGVINTASVAFFDQGTQGSASKGAIVGMTLPIARDLA 180
QY 188 PIGIRVMTIAPGLTGTPLTSLPEKVCNFTLASQVPPPSRLGDPAEYAHVQAITE 247
DB 181 RFGIRVMTIAPGLTGTPLTSLPEKVCNFTLASQVPPPSRLGDPAEYAHVQAITE 240
QY 248 GEVIRLDGAI RM 259
DB 241 GEVIRLDGAI RM 252

RESULT 3

AG3611
3-oxoacyl-(acyl-carrier protein) reductase (EC 1.1.1.100) [imported] - *Brucella melit*
C:Species: *Brucella melitensis*
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C:Accession: AG3611
R.DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
J.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melit*
A:Reference number: AD3252; PMID:11736688
A:Accession: AG3611
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-255 <RUP>
A:Cross-references: GB:AE008918; PIDN:AAL54058.1; PID:g17985013; GSPDB:GN00191
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME110816
A:Map position: 11
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: oxidoreductase

Query Match

54.3%; Score 711; DB 2; Length 255;
Best Local Similarity 57.1%; Pred. No. 1.2e-48;
Matches 144; Conservative 37; Mismatches 69; Indels 2; Gaps 1;

QY 8 VKGLVAVITGGASGLGATAEERLYVGOGASAVLDDLPNSGGEAQAOKKLGNNCVAPADYTS 67
DB 3 IENRVFLITGGASGLGAASVAKAVLLDVNAEAGAKALGASARFQRTYAS 62
QY 68 EKDVTALALAKGKFGNVDAVNCAGIAVASKTYNKKGGTHTLEDFQRYLVNVL 127
DB 63 DTDGKAALAALEAFSRDVTYVNCAGVAPGKY--LGRGKHKEETTRTISINLVGSPN 120
QY 128 VIRLVAGMGQNEPDGQGRVITNTASVAEFEGOVQAAYASAKSGIVMTLPIARDLA 187
DB 121 MLRLAAEAMSGQPDGEGRGVINTASVAFFDQGTQGSASKGAIVGMTLPIARDLA 180
QY 188 PIGIRVMTIAPGLTGTPLTSLPEKVCNFTLASQVPPPSRLGDPAEYAHVQAITE 247
DB 181 RFGIRVMTIAPGLTGTPLTSLPEKVCNFTLASQVPPPSRLGDPAEYAHVQAITE 240
QY 248 GEVIRLDGAI RM 259
DB 241 GEVIRLDGAI RM 252

RESULT 4

AT0534

Thu Jun 26 06:55:12 2003

us-09-931-186-8.rpr

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 14:23:47 ; Search time 15.6667 seconds

(without alignments)
1601.559 Million cell updates/sec

Title: US-09-931-186-8

Sequence: 1 MAAACRSYKGLAVITGAS.....ENPLNGEVIRLDGAIKMP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	748	57.1	258 2	T20484
2	720	55.0	255 2	H83326
3	711	54.3	255 2	AG3611
4	671.5	51.3	250 2	A70554
5	670	51.2	255 2	H95360
6	642	49.0	257 2	F97531
7	642	49.0	257 2	AG2750
8	595	45.5	260 2	C87264
9	383.5	29.3	247 2	E70740
10	383.5	27.1	252 2	F83098
11	343.5	26.2	249 2	F97338
12	341	26.1	246 2	H72219
13	335.5	25.6	297 2	T51084
14	334.5	25.6	291 2	AH2042
15	334	25.5	320 2	S22450
16	333.5	25.5	246 2	C83961
17	332	25.4	246 2	H84136
18	328.5	25.1	248 2	F82128
19	326.5	24.9	243 2	E97919
20	325.5	24.9	243 2	G95048
21	324.5	24.8	243 2	F86721
22	324.5	24.8	260 2	T36846
23	317	24.2	299 2	D90481
24	314.5	24.0	259 2	H98137
25	314.5	24.0	259 2	A13149
26	313.5	23.9	240 2	H75014
27	313.5	23.9	247 2	S77280
28	313.5	23.9	260 1	A48154
29	311.5	23.8	296 2	E87260
30	311	23.8		F82776
31	311	23.8		AB3545
32	310	23.7		T11579
33	309.5	23.6		AB0195
34	309.5	23.6		A69621
35	309	23.6		AG3121
36	309	23.6		H98165
37	306	23.4		A10406
38	305	23.3		H70758
39	303.5	23.2		AG1300
40	303	23.1		H98258
41	303	23.1		A13025
42	301.5	23.0		AG1672
43	301	23.0		S39737
44	300.5	22.9		T26723
45	300	22.9		S47054
46	299	22.8		S10707
47	298	22.8		B90495
48	296.5	22.7		C70885
49	296	22.6		AE3517
50	294	22.5		H84288
51	294	22.5		T36396
52	292	22.3		B37762
53	291.5	22.3		T12051
54	291	22.2		D95284
55	290.5	22.2		H70447
56	290	22.2		AG3359
57	289.5	22.1		B42147
58	288	22.0		AB0812
59	287.5	22.0		RDALAE
60	287.5	22.0		T46064
61	286.5	21.9		G90812
62	286.5	21.9		C85672
63	285.5	21.8		G75333
64	285	21.8		G82644
65	284.5	21.7		E72427
66	284.5	21.7		A72355
67	283.5	21.7		AD0642
68	283.5	21.7		B86737
69	282.5	21.6		A99950
70	282.5	21.6		C87474
71	281.5	21.5		DEKCMG
72	281	21.5		D72377
73	279.5	21.4		S06998
74	279.5	21.4		F81695
75	279	21.3		F87312
76	279	21.3		B89773
77	278	21.2		B97588
78	278	21.2		AG2809
79	277.5	21.2		D63825
80	277	21.2		F82954
81	276	21.1		A31841
82	276	21.1		A65017
83	276	21.1		A91041
84	276	21.1		D85885
85	275.5	21.0		T44351
86	275	21.0		S29278
87	275	21.0		B67378
88	274.5	21.0		B97223
89	274.5	20.8		T44434
90	272.5	20.8		C83378
91	272.5	20.8		G72389
92	272	20.8		E95903
93	272	20.8		S01237
94	272	20.8		S22416
95	270.5	20.7		S75021
96	270.5	20.7		D97325
97	270.5	20.6		B89896
98	269.5	20.6		C87408
99	269.5	20.6		S25079
100	269.5	20.6		

3-oxoacyl-(ACP) re
toluenesulfonate z
probable short cha
3-oxoacyl-(acyl-ca
3-oxoacyl-(acyl-ca
dehydrogenase Atu4
3-oxoacyl-(acyl-ca
probable dehydroge
probable fabG3 pro
3-ketoacyl-acyl ca
3-oxoacyl-(acyl-ca
3-oxoacyl-(acyl-ca
glucose 1-dehydrog
hypothetical prote
20beta-hydroxyster
hypothetical prote
probable dehydroge
3-oxoacyl-(acyl-ca
probable short cha
bile acid 7-dehydr
3-oxoacyl-(acyl-ca
probable [imported
glucose 1-dehydrog
3-oxoacyl-(acyl-ca
probable oxidoredu
acetoacetyl-CoA re
short-chain alcoh
3-oxoacyl-(acyl-ca
3-oxoacyl-(acyl-ca
3-oxoacyl-(acyl car
2,5-dichloro-2,5-c
oxidoreductase, sh
oxidoreductase, sh
3-oxoacyl-(acyl-ca
acetoaldehyde
hypothetical prote
hypothetical prote
acetoacetyl-CoA re
oxidoreductase, sh
acetoacetyl-CoA re
3-oxoacyl-(acyl ca
acetoacetyl-CoA re
acetoaldehyde
oxidoreductase, sh
3-oxoacyl-(acyl-ca
3-oxoacyl-(acyl-ca
3-oxoacyl-(acyl car
2,5-dichloro-2,5-c
oxidoreductase, sh
oxidoreductase, sh
3-oxoacyl-(acyl-ca
acetoaldehyde
hypothetical prote
hypothetical prote
acetoacetyl-CoA re
oxidoreductase, sh
acetoacetyl-CoA re
3-oxoacyl-(acyl ca
acetoacetyl-CoA re
acetoaldehyde
oxidoreductase, sh
3-oxoacyl-(acyl-ca
3-oxoacyl-(acyl-ca
3-oxoacyl-(acyl car
gluconate 5-dehydr
monensin polyketid

PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
Hypothetical protein; Oxidoreductase; NADP; Complete proteome.
NM_BIND 9 NADP (BY SIMILARITY).
FT ACT_SITE 153 153
FT CONFLICT 130 136 RGGGVIT -> TRWRSDH (IN REF. 1).
SQ SEQUENCE 256 AA; 28078 MW; D68160B1D7980C6B CRC64;
Query Match 21.7%; Score 284.5; DB 1; Length 256;
Best Local Similarity 30.7%; Pred. No. 3e-15;
Matches 83; Conservative 45; Mismatches 105; Indels 37; Gaps 8;
QY 8 VKGLVAVITGASGLGATARIIVGOGASAVLLDLPNSG--EAQAKLGNNCFAPAD 64
DB 2 LEKVAIVVTGGGGIGAIQAQLFAENGCKYVIAIDDEAGVEREEMLRERGLDVTFFKTD 61
QY 65 VTSEKDVQTALAKKGFGRDVAVNGAGIYASVSKTYNKKQTHLEDFQRYLDVNLNG 124
DB 62 VADENSVMNMYKRTVEIYGVDAVNAVAWSVKSIFE-----RPLEMERVIRVNLTG 115
QY 125 TPNVIRLVAGEMGQNEPDGQGRVYINTASVAFEGOVGOAAYSASKGIVGNTLPPIAR 184
DB 116 PYICSRCAEMIK---RGS--GVILINASTRAFOSEPDEPYASKGGLVALTHSLAV 169
QY 185 DLAPIGIRVXTIAGLFGT-----PLTSLPEKYCNFLASQVFFPSRLGDPAY 233
DB 170 SLSEYHIRVVISISPGWIEISEMKKSLRKRPDLERPIDHE-----QHP--AGRVGNPLDI 221
QY 234 AHLVQAIENP---FLNGEVIRLDGAIKRMQ 260
DB 222 AHLCEFLADDEKAGFITGTNFIYDGMIVK 251

Search completed: June 23, 2003, 14:29:24
Job time : 8.83333 secs

Matches 81; Conservative 45; Mismatches 109; Indels 19; Gaps 7;

QY 12 VAVITGASGLGATLAEPLVGGASAVLLDLPNSGGE---AQAAGKGNCCVAPADYVS 67
 DB 5 IAVTGGMGSTGALICORLAKDEFRVYAGCGPSPREKLEQOKALGDFIASEGNVAD 64
 QY 68 EKDVOALALAKGKEGVDAVAVNCAGIAVASKTYNLKKGQTHLEDFORVLDVNLMTN 127
 DB 65 WDSKTAFADKYKSEVGEVDYLLNNAGI---TRDYVEFK---MTRADWDAYIDTNLTSLPN 118
 QY 128 VIRVAGEMQNEPDGCGGVITNTASVAFEGVGQAAYSASKGGIVGNTPIARDLA 187
 DB 119 VTKQVIGMA---DREM--GRIVNISVNGKQGEQGYNTAKAGLHFTMALAQEVA 172
 QY 188 PIGIRVMTIAPGLTGLTSLPEKVCNFTLASOVPEPSRLGDPAEVAHLVQAII--ENPF 245
 DB 173 TKGTAVNTVSPGYIATDMVKAIRQDVLDKIATIPV-KRLGLEPFIASICAWLSSESGF 231
 QY 246 LNGEVIRLDGAIRM 259
 DB 232 STGADFSLNGGLHM 245

RESULT 24

PHAB_ACISP STANDARD; PRT: 248 AA.
 AC P50203; 01-NOV-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE Acetoacetyl-CoA reductase (EC 1.1.1.36).
 GN PHAB.
 OS Acinetobacter sp. (strain RA3849).
 CC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
 CC Acinetobacter.
 CC NCBI_TaxID=472;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95362679; PubMed=7635832;
 RA Schembri M.A., Bayly R.C., Davies J.K.;
 RT "Phosphate concentration regulates transcription of the Acinetobacter
 polyhydroxyalkanoic acid biosynthetic genes";
 RL J. Bacteriol. 177:4501-4507(1995).
 CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxyacyl-CoA + NADP(+) = 3-oxoacyl-CoA + NADPH.
 CC -1- PATHWAY: Polyhydroxyalkanoic acid biosynthesis; second step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SCR) FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

CC EMBL: U37761; AAA99472.1; -
 DR HSSP: P19992; IHDC.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 CC Oxidoreductase; NADP.
 KW NP_BIND 9
 FT ACT_SITE 155
 FT SEQUENCE 248 AA; 26727 MW; 850E0DC659795123 CRC64;
 SQ

Query Match 21.8%; Score 286; DB 1; Length 248;
 Best Local Similarity 31.5%; Pred. No. 2,2e-15;
 Matches 81; Conservative 47; Mismatches 105; Indels 24; Gaps 7;

QY 12 VAVITGASGLGATLAEPLVGGASAVLLDLPNSGGEAQAAGKGNCCVAPADYVS 64
 DB 6 VALTVGALGGIGISEICRLQVLAGYKIITVPRE--EDREKQWQISEGFDQSDVREVLTD 63
 QY 65 VSEKDVOALALAKGKEGVDAVAVNCAGIAVASKTYNLKKGQTHLEDFORVLDVNLMTN 124
 DB 64 LNNHRAAALAIQDEALAEGRVDVLYNNAGI---TRDAIFKK---MSYQMGQVIDTNLKT 117
 QY 125 TENVIRLVAGEMQNEPDGCGGVITNTASVAFEGVGQAAYSASKGGIVGNTPIAR 184
 DB 118 LEFTVQPVYENKMLEO-----KSGRIVNISSVNGKQGEQGYNTAKAGLHFTMALAQEVA 171
 QY 185 DLAPIGIRVMTIAPGLTGLTSLPEKVCNFTLASOVPEPSRLGDPAEVAHLVQAII--EE 242
 DB 172 EGARSNLCVNVVAPGTYATPVTAKREDYIKSTEQIFL-QRLAAPALIAAVMTLVSEH 230
 QY 243 NPELNGEVIRLDGAIRM 259
 DB 231 GAVTGETSLNGGLYM 247

RESULT 25

Y019_THEMEA STANDARD; PRT: 256 AA.
 ID Y019_THEMEA
 AC O56318; 01-NOV-1997 (Rel. 35, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative oxidoreductase TM0019 (EC 1.-.-.-).
 GN TM0019.
 OS Thermotoga maritima.
 CC Bacteria; Thermotogae; Thermotogales;
 CC Thermotogaceae; Thermotoga.
 CC NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=96125254; PubMed=8550425;
 RA Kletzin A., Adams M.;
 RT "Molecular and phylogenetic characterization of pyruvate and 2-ketoglutarate ferredoxin oxidoreductases from Pyrococcus furiosus and pyruvate ferredoxin oxidoreductase from Thermotoga maritima";
 RL J. Bacteriol. 178:248-257(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum M.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima";
 RL Nature 399:323-329(1999).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SCR) FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

CC EMBL: X85171; CAAS9459.1; -
 DR EMBL: AE001690; MAD35113.1; -
 DR HSSP: O70351; IEGW.
 DR TIGR: TM0019; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.

01-OCT-1994 (Rel. 30, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Oxidoreductase ucpa (EC 1.-.-.-).
GN ucpa OR STM2445 OR ST12682.
OS Salmonella typhimurium, and
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
CN NCBI_Taxid=602, 601,
RX [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=L72 / SGC1412 / ATCC 700720;
RX MEDLINE=21534945; PubMed=11677609;
RA McClelland M., Sanderson R.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali T., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT L72."
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE OF 204-263 FROM N.A.
RC SPECIES=S.typhimurium;
RX MEDLINE=91358382; PubMed=1909324;
RA Hryniewicz M.M., Kredich N.M.;
RT "The cysP promoter of Salmonella typhimurium: characterization of two
RT binding sites for CysB protein, studies of in vivo transcription
RT initiation, and demonstration of the anti-inducer effects of
RT thiosulfate".
RL Bacteriol. 173:5876-5886(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parthall J., Dougan A.G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahina M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Conerton P.,
RA Croxin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holyoak S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18".
RL Nature 413:848-852(2001).
RN -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
RN (SDR) FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see [http://www.isb-sib.ch/announce/
CC or_send_an_email_to_license@isb-sib.ch](http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch)).
CC
CC EMBL, AE008810; A121339.1; -;
CC EMBL, AL627274; CAD07676.1; -;
CC PIR, A38121; A38121.
CC StyGene; SG10424; ucpa.
DR InterPro; IPR002198; ADH_SHORT.
DR PROSITE; PS00061; ADH_SHORT; FALSE NEG.
KW Oxidoreductase; Complete proteome.
FT CONFLICT 218 218 L -> M (IN REF. 2).
FT CONFLICT 258 258 S -> T (IN REF. 2).
FT CONFLICT 263 263 V -> I (IN REF. 2).
SQ SEQUENCE 263 AA; 27870 MW; 818236CADD94D534E CRC64;

```

OY      10 GLVAIVITGGAGSGILAAEALVGOAGSAVLLDLPNSGGEGQAKT-----GNNCFAP 62
Db      6 GKXALLINGAGSGIGEGTARVFARHAGNALLDLDISD-----ETIEKLDELGGSGHCTAVK 60
OY      63 ADVTSEVDVCTALALAKGKRGFRDVAVNCGIAYASTYLLKKGGCHTLEDPRVLVDVL 122
Db      61 ADVADFEASVQAAVARAKETEGRIDILLVNNAGVCRLEGNFLDMSE-----EDRDFHIDINT 114
OY      123 MGFENFVRLVAGEGQNEPDGQGRGVIINTASYAA-FEGQVQQAASAKSGIGVMTLP 181
Db      115 KGVANNVAKVLPPEIKRKD-----GRTVMSSVYTGDMVADPQETVALSKKAIIVGLTSS 168
OY      182 IARDLAPIGIRVMTIAPGLFETPLTSL-----PEKCNFLASGVPPPSNLGPAPX 233
Db      169 LAVEYASGIRKRVNACICGVYTRPAEESIBAROSNPDPEVSLTEMAKAIPL-RLADPLEY 227
OY      234 AHLVC--AIIENPFLNGEIVRLDG 255
Db      228 GELAAFLASDESSVLTGTQNVIDG 251

RESULT 23
PHEB_ALCEU
ID      PHEB_ALCEU      STANDARD;      PRT;      246 AA.
AC      P14697:
DT      01-APR-1990 (Rel. 14, Created)
DT      01-APR-1990 (Rel. 14, Last sequence update)
DT      01-JUN-2002 (Rel. 41, Last annotation update)
DE      Acetoacetyl-CoA reductase (EC 1.1.1.36).
GN      PHEB.
OC      Alcaligenes eutrophus (Ralstonia eutropha).
OC      Bacteria; Proteobacteria; beta subdivision; Ralstonia group.
OC      Ralstonia.
OX      NCBI_taxid=510;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      STRAIN=H16 / DSM 428 / ATCC 17699.
RX      MEDLINE=89359355; PubMed=2670935;
RA      Peoples O.P., Slnsky A.J.;
RT      'Poly-beta-hydroxybutyrate biosynthesis in Alcaligenes eutrophus H16.
RT      characterization of the genes encoding beta-ketothiolase and
RT      acetoacetyl-CoA reductase.'
RL      J. Biol. Chem. 264:15295-15297(1989).
CC      -1- CATALYTIC ACTIVITY: (R)-3-hydroxyacyl-CoA + NADP(+) = 3-oxoacyl-
CC      CoA + NADPH.
CC      -1- PATHWAY: Poly-beta-hydroxybutyrate biosynthesis; second step.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC      (SDR) FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; J04987; AAA21973.1; .
DR      PIR; B34340; RDALAE.
DR      HSSP; 070351; 1E3S.
DR      InterPro: IPR002198; ADH_short.
DR      Pfam; PF00106; adh_short; 1.
DR      PRINTS; PRO0080; SDRFAMILY.
DR      PROSITE; PS00061; ADH_SHORT; 1.
KM      Oxidoreductase; NADP; PDB biosynthesis.
FM      NP_BIND      8      32      NADP (BY SIMILARITY).
FT      ACT_SITE      153      153      BY SIMILARITY.
SQ      SEQUENCE      246 AA; 26370 MW; ADG733E05FC06 CRC64;

Query Match      22.0%; Score 287.5; DB 1; Length 246;
Best Local Similarity      31.9%; Pred.No. 1.7e-15;

```

CC modified by non-profit institutions as long as its content is in no way
CC used and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: AE000752; AAC07575.1; -
DR HSSP: P50163; 2AE1.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT.1.
DR Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
FT NP_BIND 12 36 NADP (BY SIMILARITY).
FT ACT_SITE 157 157 BY SIMILARITY.
SQ SEQUENCE 248 AA; 26867 MW; 5CFDEB9AD83F2C5 CRC64;

Query Match 22.2%; Score 290.5; DB 1; Length 248;
Best Local Similarity 30.0%; Pred. No. 1e-15; Indels 21; Gaps 6;
Matches 77; Conservative 50; Mismatches 109;

QY 8 VKGLVAVITGSGASGLIATARLVGOGASAVLLDLPSNGGEAQAQKILGN---NCVFAPA 63
DB 5 LOGVSLVITGSGTRIGRAIAEKLASAGSVITIGTSGERAKAAVEETANKYGVKAGVEM 64
QY 64 DYTEKDVQYATLALAKKFGVDVAVNCAGIAVASKTYNKKGGTHLEDFORLYDNL 123
DB 65 NLISEESTINKAFEEIYNLDGIDILVNNAGITTRDKLFLRM-----SLDMEVLYANKLT 118
QY 124 GTFVYIRLVAGMGONPEPDGGR-GYIINTASVAEFGVGAAYASKGGIVGMLPT 182
DB 119 GTFVLTQNSLRKMK-----QWGRIVNIVSSVYGFTGVNGVYSTTRAGLIGFVKSL 171
QY 183 ARDLAPIRVMTAPGLFGTFLTLSPKXCNFLASGPSPPSRLGPAEVAHLYQAITE 242
DB 172 AKELAPRVNLVNAVAPGFETDMTRAVLSSEIKOKYKEQIPL-GRFSPSEVANYVFLCS 230
QY 243 N--PFINGEVIRLDGAI 257
DB 231 ELASVITGEVIVHNGM 247

RESULT 21
FABG_ECOLI STANDARD; PRT; 244 AA.
ID FABG_ECOLI STANDARD; PRT; 244 AA.
AC P25716; P78221; (Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (Ec 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
GN GN B1093.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE-92210530; PubMed-1556094;
RA Rawlings M., Cronan J.E. Jr.;
RT "The gene encoding Escherichia coli acyl carrier protein lies within a cluster of fatty acid biosynthetic genes."
RL J. Biol. Chem. 267:5751-5754(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE-97426617; PubMed-9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."

[3]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE-97061202; PubMed-8905232;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
RA "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."
RT DNA Res 3:137-155(1996).
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
CC This SWISS-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL: M84991; AAA3739.1; -
DR EMBL: AE000210; AAC74177.1; -
DR EMBL: D90745; BAA35901.1; -
DR PIR: B42147; B42147.
DR HSSP: P29132; 1DFT.
DR EcGene: EG11318; fabG.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT.1.
DR Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
FT NP_BIND 10 34 NADP (BY SIMILARITY).
FT ACT_SITE 151 151 BY SIMILARITY.
FT CONFLICT 30 30 A -> G (IN REF. 1).
FT CONFLICT 30 30 A -> G (IN REF. 1).
SQ SEQUENCE 244 AA; 25560 MW; 48EC1F2A7FEEDF9 CRC64;

Query Match 22.1%; Score 289.5; DB 1; Length 244;
Best Local Similarity 30.0%; Pred. No. 1.2e-15; Indels 15; Gaps 4;
Matches 76; Conservative 50; Mismatches 112;

QY 9 KGLVAVITGSGASGLIATARLVGOGASAVLLDLPSNGGEAQAQKILGNVCAPADVISE 68
DB 4 EGRALVTVGASRGIGRAIAETLAARGKAVIGTATSENGAQAISDYLGANGKGLMLNVDP 63
QY 69 KDYQATLALAKKFGFRDVAVNCAGIAVASKTYNKKGGTHLEDFORLYDNLVLMSTENV 128
DB 64 ASIESVLEKIRAFEGVEDILVNNAGITRDMLRKMD-----EENNDIETNLSVFL 117
QY 129 IRLVAGMGONPEPDGGRGVIIINTASVAEFGVGAAYASKGGIVGNTLPIDRLAP 188
DB 118 SKAYMRAMMK-----RHRITITGSGVGTMGNGGANYAAKAGLIGFSKSLAREVAS 171
QY 189 IGRVMTIAPGLGTPLTLSPKXCNFLASQVPPSPRLGPAEVAHLYQ--AIENPFL 246
DB 172 RGIIVNVAVAPGFETDMTRALSDQRAIGIAQVP-AGRIGAGQEIANAFAVFLASDEAYI 230
QY 247 NGEVIRLDGAI 259
DB 231 TGETLVHNGM 243

RESULT 22
UCPA_SALTY STANDARD; PRT; 263 AA.
ID UCPA_SALTY STANDARD; PRT; 263 AA.
AC P37441;
RT "The complete genome sequence of Escherichia coli K-12."

DR PIR: A28212; A28212.
 DR PIR: A26938; A26938.
 DR PIR: B37762; B37762.
 DR HSSP: P19992; 1HDC.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 DR OXidoreductase; NAD; Bile acid catabolism; Multigene family.
 FT NP_BIND 7 13 NAD (POTENTIAL).
 FT NP_BIND 32 36 NAD (POTENTIAL).
 FT ACT_SITE 157 157 BY SIMILARITY.
 FT CONFLICT 159 162 TSKA -> YOGG (IN REF. 2).
 SQ SEQUENCE 249 AA; 26658 MW; 084E380921D72C93 CRC64;

Query Match 22.3%; Score 292; DB 1; Length 249;
 Best Local Similarity 30.7%; Pred. No. 7.7e-16;
 Matches 83; Conservative 45; Mismatches 98; Indels 44; Gaps 10;

QY 8 VKGLVAVITGSGASGLTAERLVGOGASAVLLDLPNSGGE-----AQAKK----- 53
 DB 4 VQDKITITGSTRIGFPAALFLENGAKVSIF-----GTOGEVDTALAQLELPEE 57
 QY 54 --LGNVCYFADYTSKDVQATALAKKFGKRVDAVNCAGIYASRTYNLKKGQHTL 111
 DB 58 EVLG---FAP-DLTSRDVAAGVTAOKIGRLDVNINNGITMNSVFSKVE----- 106
 QY 112 EDFQVLDVNMGTFFNIRLVAGMGONPDQGGQGVIIINTASVAEFEGVGQAAYSAS 171
 DB 107 EDFKINDINNVGFN-----GAMSAVQCKDAKQGIITIASVTGIGSLSIGYPTS 160
 QY 172 KGIIVGMLPTARDIAPGIRVMTIAPGLFTPLTSLPEVCNVLASQVFPRLDPA 231
 DB 161 KAGVIGLHGLGREIRNRNVGAPGVDTDMKGLPELIDYLTLPK-KRMKPE 219
 QY 232 EYAHVQAIIENPFLNG---EVIRLDGAIR 258
 DB 220 EIAN-VYLFASDLASGITATTISVDGAYR 248

RESULT 19

FABG_VIBHA STANDARD: PRT; 244 AA.

ID FABG_VIBHA STANDARD: PRT; 244 AA.
 AC P55336;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
 DE FABG.
 GN Vibri. harveyi.
 OS Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibri.

OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibri.
 OX NCBI_Taxid=665;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=B392;
 RX MEDLINE=96134997; PubMed=8550484;
 RA Shen Z., Byers D.M.;
 RT Isolation of Vibri. harveyi acyl carrier protein and the fabg, acpP,
 RT and fab genes involved in fatty acid biosynthesis.";

RL J. Bacteriol. 178:571-573(1996).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: U39441; AAC43589.1; -
 DR HSSP: P19992; 1HDC.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 DR Fatty acid biosynthesis; Oxidoreductase; NADP.
 FT NP_BIND 10 34 NADP (BY SIMILARITY).
 FT ACT_SITE 151 151 BY SIMILARITY.
 SQ SEQUENCE 244 AA; 25519 MW; FC41A1C538CDAAA CRC64;

Query Match 22.3%; Score 291.5; DB 1; Length 244;
 Best Local Similarity 29.8%; Pred. No. 8.3e-16;
 Matches 76; Conservative 51; Mismatches 113; Indels 15; Gaps 4;

QY 7 SVKGLVAVITGSGASGLTAERLVGOGASAVLLDLPNSGGEQAOKKLGNNCVFAPADVT 66
 DB 2 NIEGKIALVYGASRGIGRAIAELVGRATVIGTATSEGAALISYLENGKGLALANT 61
 QY 67 SEKDVOFALALAKKFGKRVDAVNCAGIYASRTYNLKKGQHTLEDFOVLDVNLMTG 126
 DB 62 DVEISIEATLKTINDECGAIDILVNNAGITRDNLMMKRD-----DEMNDIINTNLTPIY 115
 QY 127 NVIRLVAGMGONPDQGGQGVIIINTASVAEFEGVGQAAYSASKGIIVGMLPTARDL 186
 DB 116 RMSKAVLRGMMK-----FAGRIIVGSGVGTMGAGQNTNAAAGVIGTKSKAREY 169
 QY 187 APIGIRMTAPGLFTPLTSLPEVCNVLASQVFPRLDPAEYAHLY--QALTEPP 244
 DB 170 ASRGVIVNYIYAPFIEIDMKALNDQRAATLSNV-AGRLGDFRIASAVVFLASPEAA 228
 QY 245 FLNGEVIRLDGAIRM 259
 DB 229 YITGETLHVNGMYM 243

RESULT 20

FABG_AQUAE STANDARD: PRT; 248 AA.

ID FABG_AQUAE STANDARD: PRT; 248 AA.
 AC O67610;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
 DE FABG OR AQ_1716.
 GN Aquifex aeolicus.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
 OC Aquifex.

CC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
 OX NCBI_Taxid=63363;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=V95;
 RX MEDLINE=96196666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aulay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus.";

RL Nature 392:353-358(1998).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial

QY 243 NPLNGEVIRLDG 255
 Db 229 SSVYTGAEIADVG 241

RESULT 17

Y4VL_RHISN STANDARD; PRT; 548 AA.

AC Q53217;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Putative short-chain type dehydrogenase/reductase Y4VI (EC 1.-.-.-).
 GN Y4VI.

OS Rhizobium sp. (strain NGR334).

OC Plasmid sym PNGR234a.

CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

CC Rhizobiaceae; Rhizobium.

OX NCBI_taxid=394;

RM [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=97305956; PubMed=9163424;

RA Freilberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,

RA Perret X.;

RT "Molecular basis of symbiosis between Rhizobium and legumes.";

RL Nature 387:394-401(1997).

RM [2]

RP SEQUENCE FROM N.A.

RA MEDLINE=96389014; PubMed=8796346;

RA Freilberg C., Perret X., Broughton W.J., Rosenthal A.;

RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.

RT NGR34 using dye terminators and a thermostable 'sequenase': a

RT beginning.";

RL Genome Res. 6:590-600(1996).

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

CC (SDR) FAMILY. CONTAINS TWO DOMAINS.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL: 268203; CA92424.1; ALT_INT.

DR EMBL: AE00101; AAB91897.1; -.

DR HSP; P50163; ZAE1.

DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short; 2.

DR PROSITE: PS00061; ADH_SHORT; 1.

KW Hypothetical protein; Oxidoreductase; Plasmid; Repeat;

KW Multifunctional enzyme.

FT DOMAIN 1 250

FT DOMAIN 271 548

FT NP_BIND 12 37

FT ACT_SITE 154 154

FT NP_BIND 280 304

FT ACT_SITE 420 420

FT ACT_SITE 420 420

SEQUENCE 548 AA; 57593 MW; 39959805DP17C23F CQC64;

Query Match 22.5%; Score 294.5; DB 1; Length 548;

Best Local Similarity 33.6%; Pred. No. 1.2e-15;

Matches 86; Conservative 41; Mismatches 100; Indels 29; Gaps 8;

QY 10 GVAVTGASGLGATLAEKLVGOGASAVLIDLPNSGGEAQAQKLNCCVAPADVTSEK 69

Db 9 GRVIVTGAAGIGALVDIFANDDVAVVDLPSSGVIELGQNGEHLGLEVDVSD 68

QY 70 DVQATLAKKGFGRVAVVNCAGT---AVASKTYNKKGGTHLEDFORLVNMG 125

Db 69 DVVALEALKERKFRSIEVLVNNAGIGPTMAATADT-----ALDFORALAINLGA 119

QY 126 FNVIRLVAGEMQNPDOGGQGVYIINTASVAAEQVGAAYASAKSGIVGMPLIARD 185
 Db 120 YSVACETAKLM---KFG-----AIVNNAASLAGLGNKRSAYASAKSLSTRKLACR 171

QY 186 LAPGIRVKTAPGLFGPPLTSLPEKY-----CNFLASQVPPPSLSPAPAYAHLYO--A 239

Db 172 WASRGIRVAVAPGAVHRTPEVAEL-ERAGKIDVSAIRRVPL-GRIPARDEIARVPLA 229

QY 240 ILENPFLNGEVIRLDG 255

Db 230 SNAQASTIGSTLVVDG 245

RESULT 18

BA7L_EUBSP STANDARD; PRT; 249 AA.

AC P07914;

DT 01-APR-1988 (Rel. 08, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE 7-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159) (Bile acid

DE 7-dehydroxylase) (7-alpha-HSDH) (Bile acid-inducible protein).

GN BA7L AND BA1A3.

OS Eubacterium sp. (strain VPI 12708).

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

CC Clostridium

OX NCBI_taxid=29347;

RM [1]

RP SEQUENCE FROM N.A. (BA1A3).

RA MEDLINE=9030548; PubMed=2376563;

RA Gopal-Srivastava R., Mallonee D.H., White W.B., Hylemon P.B.;

RT "Multiple copies of a bile acid-inducible gene in Eubacterium sp.

RT strain VPI 12708.";

RL J. Bacteriol. 172:4420-4426(1990).

RM [2]

RP SEQUENCE FROM N.A. (BA1A1).

RA MEDLINE=88197993; PubMed=2834320;

RA Coleman J.P., White W.B., Lajewski M., Hylemon P.B.;

RT "Nucleotide sequence and regulation of a gene involved in bile acid

RT 7-dehydroxylation by Eubacterium sp. strain VPI 12708.";

RL J. Bacteriol. 170:2070-2077(1988).

RM [3]

RP SEQUENCE OF 1-55 FROM N.A. (BA1A1), AND SEQUENCE OF 1-33.

RA MEDLINE=87165759; PubMed=3549693;

RA Coleman J.P., White W.B., Hylemon P.B.;

RT "Molecular cloning of bile acid 7-dehydroxylase from Eubacterium sp.

RT strain VPI 12708.";

RL J. Bacteriol. 169:1516-1521(1987).

CC -1- FUNCTION: 7-ALPHA-DEHYDROXYLATION OF CHOLIC ACID. YIELDING

CC DIOXYCHOLIC ACID AND LITHOCHOLIC ACID, RESPECTIVELY. HIGHEST

CC AFFINITY WITH TAUROCHENODEOXYCHOLIC ACID.

CC -1- CATALYTIC ACTIVITY: 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-

CC cholanoate + NAD(+) = 3-alpha,12-alpha-dihydroxy-7-oxo-5-beta-

CC cholanoate + NADH.

CC -1- PATHWAY: Bile acid catabolism.

CC -1- INDUCTION: PRESENCE OF C(24) BILE ACIDS CONTAINING A

CC 7-ALPHA-HYDROXY GROUP.

CC -1- SIMILARITY: THERE ARE THREE GENES FOR BATA PROTEINS: BA1A1 IS

CC IDENTICAL TO BA1A3 AND THERE IS 81% IDENTITY WITH BA1A2.

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

CC (SDR) FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL: M34658; AAB61155.1; -.

DR EMBL: M19654; AAB61154.1; -.

DR EMBL: M15813; AAB61153.1; -.

MEDLINE-98044033; PubMed-9384377;
 RA Kunst F., Ogatawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Beterio M.G., Bessieres P., Bolotin A., Borchet S.,
 RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Deniazo F., Devine K.M., Dusterhoft A., Enright S.D., Emmerson P.T.,
 RA Ertan K.D., Errington J., Fabret C., Ferrati E., Foulger D.,
 RA Filiz C., Fujita M., Fujita T., Funa S., Gallizi A., Galleron N.,
 RA Gilm S.Y., Glaser P., Goffeau A., Gollightly E.J., Grand C.,
 RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kunita K., Lapius A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Malet C., Medigue C.,
 RA Medina N., Melido R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetalle D., Portoullik S., Prescott A.M.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivoita C., Roche E., Roche B., Rose M., Sadale Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
 RA Sato T., Sekowska A., Serró S.J., Serró P., Shin B.S., Soldo B.,
 RA Sorokin J., Taconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terpsita P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassartoli A.,
 RA Viari A., Wambut R., Wedler E., Wedler H., Weitenegger T.,
 RA Witters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zanchin A.,
 RA "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis." Nature 390:249-256(1997).
 RL Nature 390:249-256(1997).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: X73124; GAA51638.1; -
 DR EMBL: 299123; CAB5799.1; -
 DR PIR: S39737; S39737.
 DR HSP: P50162; IAE1.
 DR Subtilisin; BG10628; ywFD.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRPFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 DR Hypothetical protein; Oxidoreductase; Complete proteome.
 KW NP_BIND 11 33 NAD OR NADP (By SIMILARITY).
 FT ACT_SITE 154 154
 SQ SEQUENCE 255 AA; 27324 MW; 20AA2259BFB8C9B CRC64;

Query Match 23.0%; Score 301; DB 1; Length 255;
 Best Local Similarity 32.7%; Pred. No. 1.6e-16;
 Matches 88; Conservative 42; Mismatches 99; Indels 46; Gaps 8;
 QY 14 VITGASGLGATTAERLVGOGASAVLLDLPNSGGAQAKKGNVCV-FAPADVTSEKYO 72
 DB 11 ITTGASGSGYAAVAFIFGQGANVVADIDEAGSAMRKENDRLHFGVDDIDIDEAQC 70
 QY 73 TALALAKGFGVADVAVNCAAGIAVASKTYNLKGGTHLEDFORVLDVNLGTFVIR- 130
 DB 71 HAVESAVHTFGGLDVILNAGIEIYAPHEM-----LSDMNKLQVNLIGMFLMSHA 124
 QY 131 ----LVAGMGONEPDGQGVITINTASVAAFEGVQGAAYSAKSGIGVMTLPIDAL 186
 DB 125 LKHEMLAAG-----KGNITNCSVSGVLVAMPDIPAYNASKGVLQILTKSMADV 172
 QY 187 APIGRVMTIAPGLFGTPLLTLSPKVCNFTL-----ASQVFPFSLGDPAEY 233
 DB 173 AKHQIRVNCVCGIITDP-----LNK-----SFLNNNGTLEIKKAKAKNPILRLGKPEEI 226
 QY 234 AHVQAALIE--NPFLNGEYIRIDGAIKQ 260
 DB 227 ANVMLFLASDLSSYMTGSAITADGGYTAQ 255
 RESULT 16
 ID 2BHD_STREX STANDARD; PRT; 255 AA.
 AC 2BHD_STREX
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE 20-beta-hydroxysteroid dehydrogenase (EC 1.1.1.53).
 OS Streptomyces exfoliatus (Streptomyces hydropneus).
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteriales;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1905;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-90306362; PubMed-2194840;
 RA Marekov L., Krook M., Joernvall H.;
 RT "Prokaryotic 20 beta-hydroxysteroid dehydrogenase is an enzyme of the
 RT 'short-chain, non-metalloenzyme' alcohol dehydrogenase type.";
 RL FEBS Lett. 266:51-54(1990).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE-92052211; PubMed-1946424;
 RA Ghosh D., Weeks C.M., Grochulski P., Duax W.L., Erman M.,
 RA Rimsay K.L., Orr J.C.;
 RT "Three-dimensional structure of holo 3 alpha,20 beta-hydroxysteroid
 RT dehydrogenase: a member of a short-chain dehydrogenase family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:10064-10068(1991).
 CC -1- CATALYTIC ACTIVITY: Androstane-3-alpha,17-beta-diol + NAD(+) = 17-
 CC beta-hydroxyandrostane-3-one + NADH.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 DR PIR: S10707; S10707.
 DR PDB: 2HSD; 31-AUG-94.
 DR PDB: 1HDC; 07-FEB-95.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRPFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 DR Oxidoreductase; NAD; Steroid metabolism; 3D-structure.
 KW NP_BIND 10 34 NAD (By SIMILARITY).
 FT ACT_SITE 152 152
 SQ SEQUENCE 255 AA; 26484 MW; 90B93CB66AA628D5 CRC64;

NP BIND 9 33 NADP (BY SIMILARITY).
 ACT SITE 154 154 BY SIMILARITY.
 FT 23 23 D -> A (IN REF. 1).
 SQ SEQUENCE 246 AA; 26282 MM; C6A391167D237DC CRC64;

Query Match 23.6%; Score 309.5; DB 1; Length 246;
 Best Local Similarity 29.7%; Pred. No. 3.3e-17;
 Matches 76; Conservative 55; Mismatches 100; Indels 25; Gaps 6;

QY 13 AVITGGASGIGLAEELVGGASAVILDLPSNGSGEQA-----KRIQNNCFAPADV 65
 DB 7 AIVTGGASGIGLAEELVGGASAVILDLPSNGSGEQA-----KRIQNNCFAPADV 63
 QY 66 TSEKDYOTATLAKKGRGVAVNAGIAVASKTYNLKGGOTHTLEDFOFVLDVNLMT 125
 DB 64 SNPEDVQNMKEITLVSFTIDILVNNAGITRDLIMMKE-----DEMDDVINILKGV 117
 QY 126 PNVIATLVAGEMGQNEPQGGQGVITNTASVAFEGVQGAASAKSGIVGTLIARD 185
 DB 118 FNCTKATVROMKQ-----RSGRITLVSVIVSGVSGNPQANTYAAAGVIGLTKSSAKE 171
 QY 186 LAPIGIVMTIAPGLFTPLTSLPERKVCNFIASQVPEPRLDPAEYAHVQAITE-- 243
 DB 172 LASNIIVNNAIAPFISTDMTDKLAKVDQDEMLKQIPL-ARFGEPSDVSSVTFILASEGA 230
 QY 244 PFLNGEVIIRLDGAIM 259
 DB 231 RYMTGQTLHDGMAV 246

RESULT 14
 YK02_MYCTU STANDARD; PRT; 260 AA.

AC Q10855; 1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 38, Last sequence update)
 DT 15-JUN-1999 (Rel. 40, Last annotation update)
 DE Putative oxidoreductase Pw2002 (EC 1.-.-.-)
 GN FABG3 OR RV2002 OR MT2058 OR MTCX39.16C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RC MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Besham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Kirogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
 RT Nature 393:537-544 (1998).
 RN [2]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN-CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Dvortack T., Weidman J., Kouri H., Gill J., Mikula A., Bishai W.;
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

CC -----
 DR EMBL; 274025; CAA98414.1; -
 DR EMBL; AE007057; AAK46335.1; -
 DR HSSP; P19992; LHDC.
 DR TIGR; MT2058; -
 DR Tuberculist; RV2002; -
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
 FT NP BIND 11 35
 FT ACT SITE 153 153
 FT CONFLICT 174 174 S -> G (IN REF. 2).
 SQ SEQUENCE 260 AA; 27030 MM; 0935A14ED36220B7 CRC64;

Query Match 23.3%; Score 305; DB 1; Length 260;
 Best Local Similarity 33.9%; Pred. No. 7.9e-17;
 Matches 85; Conservative 41; Mismatches 99; Indels 26; Gaps 5;

QY 10 GLVAVITGGASGIGLAEELVGGASAVILDLPSNGSGEQAARKLNCCVFPADVTESEK 69
 DB 7 GKVALYSGARGMGASHVAMAEKAYFGSIIDEBGKAAVALADARVYHLDVTPA 66
 QY 70 DVQATLALAKKGRGVAVNAGIAVASKTYNLKGGOTHTLEDFOFVLDVNLMTFNV 129
 DB 67 QMTAAVDVTAFAFGHLVJNNAGI-----LNTGIEDYALTEQRIIDVNLGVFGLI 120
 QY 130 RLVAGEMGQNEPQGGQGVITNTASVAFEGVQGAASAKSGIVGTLIARDLAPI 189
 DB 121 RAVV-----KPKKEKRGKSIINISIEGLAGTVACHGTAKFAVRGLTRKTALELGS 174
 QY 190 GIRVMTIAPGLFTPLTSLPERKVCNFIASQVPEPRLG---DPAEYAHV---QAITENP 244
 DB 175 GIWNSIHPLGLVTPMTDWPEDI-----FQTLGRAAPVEVSMVLYVYASDSS 225
 QY 245 FLNGEVIIRLDG 255
 DB 226 YSTGAEPFVVDG 236

RESULT 15

YWFD_BACSU STANDARD; PRT; 255 AA.

AC P39640;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical oxidoreductase ywfd (EC 1.-.-.-).
 GN YWFD OR IPA-82D.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RC MEDLINE=95020537; PubMed=7934828;
 RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W., Hulo M.F., Ionescu M., Lubochinsky B., Marcelinsky J., Mosser I., Prescecian E., Santana M., Schneider E., Schweizer J., Vertes A., Rapoport G., Dancu A.;
 RA "Bacillus subtilis genome project: cloning and sequencing of the 97 kb region from 325 degrees to 333 degrees."
 RT Mol. Microbiol. 10:371-384 (1993).
 RN [2]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN-168;

RP SEQUENCE FROM N.A.

RX STRAIN-168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Acedo V., Bertero M.G., Bessieres P., Bolotin A., Borcherdt S.,
RA Boris R., Boursier L., Brans A., Brun M., Bridgell S.C., Bron S.,
RA Brouillet S., Busch U.J., Conerton J.F., Cummings N.V., Carter N.M.,
RA Choi S.K., Codani J.M., Dusterhoft A., Erlich S.D., Emerson P.T.,
RA Denizot F., Devine K.M., Conteroth A., Erlich S.D., Foulger D.,
RA Etian K.D., Errington J., Fabre C., Ferrari E., Galleron N.,
RA Fritz C., Fujita M., Fujita Y., Funo S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holtsappel S., Hosono S., Hullio M.F., Itaya M., Jones L.,
RA Joris B., Kamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapilus A., Lardinios S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Neone D., O'Reilly M., Ogawa K., Ojigawa A., Outega B., Park S.H.,
RA Parro V., Pohlt T.M., Portetelle D., Potwolkil S., Prescott A.M.,
RA Pressman E., Puic P., Putnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Riyolta C., Rocha E., Roche B., Rose W., Sadie Y.,
RA Sato T., Scanlan E., Schleich S., Schrotter R., Scottone F.,
RA Setighuchi J., Selowska A., Seror S.J., Serfor P., Shin B.S., Soldo B.,
RA Sorokin M., Tacconi E., Takegi T., Takahashi H., Takemaru K.,
RA Torachi M., Tanakoshi E., Tanaka T., Terstra P., Togonni A.,
RA Tosato V., Uchiyama S., Vandenhof M., Vanlier F., Vassarotti A.,
RA Viart A., Wandut R., Wedler E., Weiler H., Welteneeger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumslein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis";
RT Nature 390:249-256(1997).

RN [3]
RN SEQUENCE OF 1-172 FROM N.A.
RP STRAIN-168;
RX MEDLINE=98195738; PubMed=9534248;
RA Foulger D., Errington J.;
RT "A 28 kbp segment from the spvVM region of the Bacillus subtilis 168
RT genome";
RL Microbiology 144:801-805(1998).

RN [4]
RN SEQUENCE OF 230-246 FROM N.A.
RC STRAIN-168;
RA Oguro A., Kasheta H., Takamatsu H., Nakamura K., Yamane K.;
RC Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: [(3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATY ACID BIOSYNTHESIS
CC PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASIS
CC (SDR) FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sdb.ch/announce/>).
CC or send an email to license@sdb-stb.ch.

DR -----
DR EMBL: U59433; AAC44307.1; -
DR EMBL: Z99112; CAB13464.1; -
DR EMBL: Y13937; CAAT4250.1; -
DR EMBL: D64116; BAA10974.1; -
DR HSSP: Q12634; 1IIEV.
DR Subtilist; BG11533; fabG.
DR InterPro; IPRO02198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PRO00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; FALSE NEG.

RETRACTED bioinformatics. Oxidoreductase NADP. Complete proteome

Db 62 NPESIEVALKATIDDEGGVDILVNNAGITRDNLMMRKE-----EEMSDIMETNLTSTF 115
 QY 127 NVIRLVAGEMGONEPDGGRGVYIINTASVAFAEGOVGAAYASASKSGIVGWTLPARDL 186
 Db 116 RLKAVLRGMMKK-----RQGRINNGSVGTMGNAGNAAKAGVIGFTKSMAREY 169
 QY 187 APGIRMTIAPGLFGPILTLSPKVCNCLASOVPPSRIGDPAREYAHYNOAIENP-- 244
 Db 170 ASKGVNTVAAPGFIETDMTKALNDEQRATVLAQVP-AGRIGDPRELASAV-AFLASPER 227
 QY 245 -FLNGEYIRLDGAIRM 259
 Db 228 AYIGETLHVNGGMYM 243

RESULT 11
 FAGL_SVNY3 STANDARD; PRT; 247 AA.

AC P73574;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase 1 (EC 1.1.1.100) (3-
 ketolacyl-acyl carrier protein reductase 1).
 GN Synechocystis sp. (strain PCC 6803).
 OS Synechocystis; Cyanobacteria; Chroococcales; Synechocystis.
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_Taxid=1148;

RA MEDLINE-97061201; PubMed-8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hikosawa M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nario K., Okumura S.,
 RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RA "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----

DR EMBL; D90907; BAA17614.1; .
 DR HSP; P50162; IAE1.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FM NP_BIND 156
 FT ACT_SITE 156
 SQ SEQUENCE 247 AA; 25724 MW; 91DBF9409C77F20 CRC64;

Query Match 23.9%; Score 313.5; DB 1; Length 247;
 Best Local Similarity 32.1%; Pred. No. 1,6e-17;
 Matches 85; Conservative 45; Mismatches 92; Indels 43; Gaps 8;

12 VAVITGASGLIATAEIRLVGG-----ASAVILDLPSNGEGEAQAKKLGNMC 58

Db 8 VALVTGASRGIGKATATALATATGMKVYVNAOSSTAADVVAEIIANGEA----- 58
 QY 59 VFAPADVISEMDYOCALALAGKRGVRVAVNCGINAVASTYMLKKQGTLPEDFQVYL 118
 Db 59 IAVQANVANAEVDOLITTLDRSRIDVYVNNAGITDILLRK-----LEDWQAVI 112
 QY 119 DVNLGTFNVIRLVAGEMGONEPDGGRGVYIINTASVAFAEGOVGAAYASASKSGIVGM 178
 Db 113 DNLGVFLCTKAVSKMLKQ-----KSGRIINTSVAGMGNPGQANYSAAKAGVIGF 166
 QY 179 TLPIARDLAPGIRMTIAPGLFGPILTLSPKVCNCLASOVPPSRIGDPAREYAHY 237
 Db 167 TKTVAKEILASRGVTVNAAPGFIATDMENLNAEPILOP-----IPL-ARYGOPEVAGTI 221
 QY 238 QAIENP--FLNGEYIRLDGAIRM 259
 Db 222 RELATDPAAAYITGTFNVNDGMYM 246

RESULT 12
 DHB8_MOUSE STANDARD; PRT; 260 AA.

AC P50171; Q60959; Q60958; Q921W2;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Estradiol 17 beta-dehydrogenase 8 (EC 1.1.1.62) (17-beta-HSD 8) (17-
 beta-dehydroxysteroid dehydrogenase 8) (K6 protein) (K6-6).
 GN HSD17B8 OR HKE6 OR H2-K6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Kidney;
 RX MEDLINE-93180832; PubMed-8441417;
 RA Aziz N., Maxwell M.M., St Jacques B., Brenner B.M.;
 RT "Downregulation of K6, a novel gene encoded within the major
 RT histocompatibility complex, in murine polycystic kidney disease.";
 RL Mol. Cell. Biol. 13:1847-1853(1993).
 RN [2]
 RN ERRATUM.
 RA Aziz N., Maxwell M.M., St Jacques B., Brenner B.M.;
 RL Mol. Cell. Biol. 13:6614-6614(1993).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE-96027630; PubMed-7559658;
 RA Maxwell M.M., Neuring J., Aziz N.,
 RT "K6 gene. Sequence and organization and aberrant regulation in
 RT murine polycystic kidney disease.";
 RL J. Biol. Chem. 270:25213-25219(1995).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP STRAIN-129/svJ;

RC Rowen L., Qin S., Madan A., Loretz C., James R., Dors M., Mix L.,
 RA Hall J., Lasky S., Hood L.;
 RT "Sequence of the mouse major histocompatibility locus class II
 RT region.";
 RL Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: USES ESTRADIOL AS ITS PREFERRED SUBSTRATE.
 CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P)(+) = estrone +
 CC NAD(P)H.
 CC -1- PATHWAY: BIOSYNTHESIS OF ESTROGENS.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A SHORT FORM (SHOWN HERE) AND A
 CC LONG FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: KIDNEY, LIVER AND MODERATELY IN SPLEEN, HEART
 CC AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

AC Q92506; Q9UIQ1;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Estradiol 17 beta-dehydrogenase 8 (EC 1.1.1.62) (17-beta-HSD 8) (17-
 beta-hydroxysteroid dehydrogenase 8) (K66 protein) (K6-6).
 GN HSD17B8 OR HKE6 OR RING2 OR FABGL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tubby B.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 3-261 FROM N.A.
 RX MEDLINE=97001166; PubMed=8812499;
 RA Ando A., Kikuchi Y., Shigenari A., Kawata H., Okamoto N., Shina T.,
 Chen L., Ikemura T., Abe K., Kimura M., Inoko H.,
 "cDNA cloning of the human homologues of the mouse K64 and K66 genes
 at the centromeric end of the human MHC region."
 RT Genomics 35:600-602(1996).
 CC -1- FUNCTION: USES ESTRADIOL AS ITS PREFERRED SUBSTRATE.
 CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P)(+) = estrone +
 NAD(P)H.
 CC -1- PATHWAY: BIOSYNTHESIS OF ESTROGENS.
 CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE LIVER AND PANCREAS,
 LOWER IN THE SKELETAL MUSCLE AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 CC CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC CC
 DR EMBL: AL031228; CAC38444.1;
 DR EMBL: DB2061; BA01529.1;
 DR HSSP: O70351; 1E6W.
 DR GeneW: HGNC:3554; HSD17B8.
 DR MIM: 601417;
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 KM Steroid biosynthesis; Oxidoreductase; NAD; Multigene family.
 FT NP_BIND 15
 FT ACT_SITE 169
 FT CONFLICT 117
 FT CONFLICT 193
 FT CONFLICT 208
 FT CONFLICT 212
 SEQUENCE 261 AA; 26974 MW; 8B8B2D7131714D71 CRC64;
 Query Match 25.4%; Score 332.5; DB 1; Length 261;
 Best Local Similarity 31.2%; Pred. No. 5.9e-19;
 Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;
 QY 8 VKGVAVITGGASGIGLATFAERLVGGASAVLLDPNSGGEAQAARKL-----GN 56
 DB 9 LRSALAVITGAGSGIGRAVSRLAGEGATVAACIDPRAADPTVRLGPGSKSGPPRGN 68
 QY 57 NCVFADVTSKEDVQTALALAKRFGK-VDVAVNCAGIAVASKTYNLKQGTHTLEDQ 115
 DB 69 HAAF-QADVSEARARCLLEGVQACFSRPPSVVASCAGITODEFLHASE-----DDWD 121
 QY 116 RVLVDVNGTFTVIVLVAGGQGNPPDGGQGRGVININAAVAFPGCVGGAAYASAKGI 175
 DB 122 KVIAVAKGTFTLVTAQAALVSN-----GCGSTIINISIVGKGVNGQVYTAASKAGV 176

QY 176 VENTLPIARDLAPIGIRVNTIAPLGGLPPLTSLPEKYCNLTASQVPPPSRLGPAEYAH 235
 DB 177 IGLTQAAELRGHRGRCNSVLPGLAFPMTOKVQKVDKITEMIPM-GRIGDEPDVAD 235
 QY 236 LVQ--AIINPFLNGEVIRLDGAIIR 259
 DB 236 VVAFLASEDSGYITGTSVEVTGGLF 261
 RESULT 10
 ID FABG_VIBCH STANDARD; PRI: 244 AA.
 AC Q9KQJ7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
 acyl carrier protein reductase).
 GN FABG OR VC2021
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 NX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SPRAIN-El For N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
 Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 Emdolaeva L.D., Vamathevan J., Bass S., Qin H., Drago I., Sellers P.,
 McDonauld L., Utterback T., Fleischmann R.D., Niemann W.C., White O.,
 Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 Fraser C.M.;
 RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae".
 RT Nature 406:477-483(2000).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 CC CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC CC
 DR EMBL: AE004276; AAF95169.1; ALT_INT.
 DR HSSP: P19992; 1HDC.
 DR TIGR: VC2021;
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 KM Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 10
 FT ACT_SITE 34
 FT ACT_SITE 151
 SEQUENCE 244 AA; 25566 MW; 9FB2B8278D7CC3CE CRC64;
 Query Match 25.1%; Score 328.5; DB 1; Length 244;
 Best Local Similarity 32.0%; Pred. No. 1.1e-18;
 Matches 82; Conservative 54; Mismatches 103; Indels 17; Gaps 5;
 QY 7 SVKGVAVITGGASGIGLATFAERLVGGASAVLLDPNSGGEAQAARKLGNVCFAPADVT 66
 DB 2 NLEKVALVVGASGIGKAIKIAELAEKAGVICTATSESGAQAISDYLGDNGKGMALNV 61
 QY 67 SEKVQYALALAKRGRVDVAVNCAGIAVASKTYNLKQGTHTLEDQVRLVDVNGMT 126

RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Hart D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RA "Evidence for lateral gene transfer between Archaea and Bacteria from
 genome sequence of *Thermococcus maritima*.";
 RL Nature 399:323-329(1999).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AE001811; AAD36790.1; -
 DR HSSP: P50162; IAEI.
 DR TIGR: TMI1724; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Fatty acid biosynthesis; Oxidoreductase; NADP: Complete proteome.
 KW NP_BIND 10 34 NADP (BY SIMILARITY).
 FT ACT_SITE 154 154 BY SIMILARITY.
 FT SEQUENCE 246 AA; 26401 MW; 8008904D28099142 CRC64;
 SQ
 Query Match 26.1%; Score 341; DB 1; Length 246;
 Best Local Similarity 33.7%; Pred. No. 1.2e-19;
 Matches 86; Conservative 47; Mismatches 104; Indels 18; Gaps 5;
 QY 8 VKGLAVITGASGLGATLAEVLVGGASAVLDPNSGGA---QAKKLGNKVPAPAD 64
 DB 3 LEGKVLITGASAGIGKATTLTLLFAQEGATVAGDISKENDSLVKEAEGPGRKVPYLL 62
 QY 65 VTSEKDVOYALALAKGKRGVAVANCAGIAVASKTYLKKQGHTEDEFOVLDVNLNG 124
 DB 63 VTDROQKEVEYKVGKGRIDVLYNNAGITRDALVAKRE-----EDMDAVINVLKG 116
 QY 125 TENVIRLVAGENGQNEPDGGRGVIINTASVAAEFGGVGAAYSASGSGIVGTLPIAR 184
 DB 117 VENVYQMVVPIRKQ-----KNGSIVAVSSVVGIGNPQNTNYSASRAVIGMTKRWAK 170
 QY 165 DLAPGIVMTAPLFGFPLTSLPEKVCNFIASQVFPSPRLGDPAPAYAHV--QAIIIE 242
 DB 171 ELAGNINRINAVAPGFITETPEKLEKARETALSRIPL-GRFGPEVAYQVILFLASDE 229
 QY 243 NFELNGEYIRLDGAI 257
 DB 230 SSYVTGVYIGIDGGL 244
 RESULT 8
 ID FABG_CUPLA STANDARD; PRT; 320 AA.
 AC P28643;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase, Chloroplast precursor
 DE (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
 GN CLKR27.
 OS Cuphea lanceolata.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Myrtales; Lythnaceae; Cuphea.
 OX NCBI_TaxID=3930;
 RN [1]
 RP SEQUENCE FROM N.A. PubMed=1376402;
 RX MEDLINE=92293104; PubMed=1376402;
 RA Klein B., Pawlowski K., Hoerlcke-Grandpierre C., Schell J.,
 RA Toepfer R.;
 RA "Isolation and characterization of a cDNA from *Cuphea lanceolata*
 RA encoding a beta-ketoacyl-ACP reductase.";
 RL Mol. Gen. Genet. 233:122-128(1992).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC
 CC PLASTIDS.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X64566; CAA45866.1; -
 DR PIR: S19832; S19832.
 DR HSSP: P50162; IAEI.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Fatty acid biosynthesis; Oxidoreductase; NADP: Chloroplast;
 KW Transf. peptidase.
 FT TRANSIT 1 61 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 62 320 NADP (BY SIMILARITY).
 FT NP_BIND 82 106 NADP (BY SIMILARITY).
 FT ACT_SITE 227 227 BY SIMILARITY.
 FT SEQUENCE 320 AA; 33103 MW; 06BAF0522B2B8C87 CRC64;
 SQ
 Query Match 25.5%; Score 334; DB 1; Length 320;
 Best Local Similarity 32.7%; Pred. No. 5.7e-19;
 Matches 87; Conservative 46; Mismatches 111; Indels 22; Gaps 6;
 QY 2 AAACRSYKGLAVITGASGLGATLAEVLVGGASAVLDPNSGGA---QAKKLGN 56
 DB 69 AGAGQSVSEPVIVTGSRGIGKALSL-GKAGCYLVAVYARSSEAEVSKIEAFAG 127
 QY 57 NCYFAPADVTSKDVOTALALAKGKRGVAVANCAGIAVASKTYLKKQGHTEDEFOV 116
 DB 128 QALTFGGDVSKEDVEAMITAYDANGTYDILVNNAGITDGLMKRKSQ-----NQE 181
 QY 117 VLDVNLNGTFNVIRLVAGENGQNEPDGGRGVIINTASVAAEFGGVGAAYSASGSGIV 176
 DB 182 VIDNLNGVFLCTQAAKIMKK-----KKGRITINIASVVGIVGNAGQANYSAAAGVY 235
 QY 177 GMTLPFARDLAPGIRVMTAPLFGFPLTSLPEKVCNFIASQVFPSPRLGDPAPAYAHV 236
 DB 236 GFTYVAREYASRNINAVAPGFISSDMSKIGDDINKILLETPL-GRYGPPEVAYGL 294
 QY 237 VQAIENP---FLNGEYIRLDGAI 259
 DB 295 VEFIAINPSSVYGVFTIDGGM 320
 RESULT 9
 ID DH8_HUMAN STANDARD; PRT; 261 AA.
 DH8_HUMAN

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA;
 RA Fu J., Chen X., Stern D., Van S. D.;
 RL Submitted (Apr.1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
 CC + NADH.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U66116; AAB57689.1; ALT_INIT.
 DR HSP: 070351; 1E6W.
 DR SWISS-2DPAGE: 008756; MOUSE.
 DR MGD: MGI:1333871; Hsdl7b10.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Oxidoreductase; NAD.
 DR NP_BIND 12
 FT ACT_SITE 168
 FT SEQUENCE 261 AA; 27418 MW; 61213B1E2839D41 CRC64;
 SQ
 Query Match 86.5%; Score 1132; DB 1; Length 261;
 Query Local Similarity 86.2%; Pred. No. 3; 3e-81;
 Matches 225; Conservative 19; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MAAACRSYKGLVAVITGASGLGIAIEKLVGGASAVLLDLPNSGGEAQAQKLGNCF 60
 DB 1 MAAVRSYKGLVAVITGASGLGIAIEKLVGGASAVLLDLPNSGGEAQAQKLGNCF 60
 QY 61 AAPVTSEKDYQTALAKGFGVDVAVNACAGAVASKTYNKKGGTHTLEDFORLVDY 120
 DB 61 AAPVTSEKDYQTALAKGFGVDVAVNACAGAVASKTYNKKGGTHTLEDFORLVDY 120
 QY 121 NLMGTFNVIRLVAGEMQNEFDQGGQGVIIINTASVAEFGQVQAASAKSGIYGMWL 180
 DB 121 NLMGTFNVIRLVAGEMQNEFDQGGQGVIIINTASVAEFGQVQAASAKSGIYGMWL 180
 QY 121 NLIGTFNVIPLVAGEMQNEFDQGGQGVIIINTASVAEFGQVQAASAKSGIYGMWL 180
 DB 121 NLIGTFNVIPLVAGEMQNEFDQGGQGVIIINTASVAEFGQVQAASAKSGIYGMWL 180
 QY 181 PIADLAPIGIRWTTIAPGLGFEPLTSLPEKVCNFTASQVPEFSRLGDPAEVAHLVQAI 240
 DB 181 PIADLAPIGIRWTTIAPGLGFEPLTSLPEKVCNFTASQVPEFSRLGDPAEVAHLVQAI 240
 QY 241 IENPFLNGEVIIRLDGAIRMOP 261
 DB 241 IENPFLNGEVIIRLDGAIRMOP 261
 RESULT 5
 HCD2_DROME STANDARD; PRT; 255 AA.
 AC 018404;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)
 DE (Scully protein).
 GN SCU OR CG7113.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A. AND KOTAGENESIS OF LEU-33 AND PHE-120.
 RC STRAIN=Canton S;
 RX MEDLINE=98252852; PubMed=9585418;
 RA Torroja L., Ortuno-Sahagun D., Ferrus A., Haemmerle B., Barbas J.A.;
 RT Scully, an essential gene of Drosophila, is homologous to mammalian
 RT mitochondrial type II L-3-hydroxyacyl-CoA dehydrogenase/amyloid-beta
 RT peptide-binding protein.
 RL J. Cell Biol. 141:1009-1018 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.Y.,
 RA Brandon R.C., Rogers J.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Abrill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borovna D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Flosser C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Idegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moschelli A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Patel J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J.D., Pui Y., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skusek M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195 (2000).
 CC -1- FUNCTION: MAY PLAY A ROLE IN GERM LINE FORMATION.
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
 CC + NADH.
 CC -1- SUBUNIT: MULTIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
 CC -1- TISSUE SPECIFICITY: FOUND IN MANY TISSUES INCLUDING CNS. HIGHEST
 CC EXPRESSION IN BOTH EMBRYONIC GONADAL PRIMORDIA AND MATURE OVARIES
 CC AND TESTES.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Y15102; CAA75377.1; -

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; AB002156; BAA19510.1; -
DR HSSP; 070351; 1E6W;
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KM Oxidoreductase; NAD; Mitochondrion.
FT NP_BIND 12 37 NAD (BY SIMILARITY).
FT ACT_SITE 168 168 BY SIMILARITY.
SQ SEQUENCE 261 AA; 27140 MW; 8C7572B6A9A49780 CRC64;

Query Match 92.1%; Score 1206; DB 1; Length 261;
Best Local Similarity 92.0%; Pred. No. 9,6e-87;
Matches 240; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGGASGLGATAEKLYGGASAVLLDLPNSGGEAOKKLGNNCYF 60
DB 1 MAACRSYKGLVAVITGGASGLGATAEKLYGGASAVLLDLPNSGGEAOKKLGNNCYF 60
QY 61 APADVSEKDYQVATLALAKGFGVDVAVNCAGIAVASKTYNKKGQTHLEDFORVLDV 120
DB 61 APADVSEKDYQVATLALAKGFGVDVAVNCAGIAVASKTYNKKGQTHLEDFORVLDV 120
QY 121 NLMGTFNIVIRIVAGEMQNEPDGQGGQGVITINTASVAFEGOVQAAYSASKGIYGMTL 180
DB 121 NLMGTFNIVIRIVAGEMQNEPDGQGGQGVITINTASVAFEGOVQAAYSASKGIYGMTL 180
QY 121 NLIGTFNIVIRIVAGEMQNEPDGQGGQGVITINTASVAFEGOVQAAYSASKGIYGMTL 180
DB 121 NLIGTFNIVIRIVAGEMQNEPDGQGGQGVITINTASVAFEGOVQAAYSASKGIYGMTL 180
QY 181 PIADLPIGIRVMTIAPGLTSLPEKYNFLASQVPPFSRLGDPAEVAHLVQAI 240
DB 181 PIADLPIGIRVMTIAPGLTSLPEKYNFLASQVPPFSRLGDPAEVAHLVQAI 240
QY 241 ENPFLNGEIVIRLDGAIKMP 261
DB 241 ENPFLNGEIVIRLDGAIKMP 261

RESULT 3
HCD2_RAT
ID HCD2_RAT STANDARD; PRT; 260 AA.

AC 070351; Q9QYD4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)
DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein).
GN HADH2 OR ERAB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Gunn-Moore F.J., Tavaire J.M.;
RT "Rattus norvegicus amyloid beta-peptide binding protein (ERAB) mRNA";
RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Yang S.-Y., He X.-Y.;
RT "Molecular cloning and characterization of the cDNA of rat brain short chain L-3-hydroxyacyl-CoA dehydrogenase.";
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC TISSUE=Brain;
RA MEDLINE=20481418; PubMed=11023795;
RA Powell A.J., Read J.A., Banfield M.J., Gunn-Moore F., Yan S.D.,
RA Justbader J., Stern A.R., Stern D.M., Brady R.L.;

RT "Recognition of structurally diverse substrates by type II
RT 3-hydroxyacyl-CoA dehydrogenase (HADH II)/amyloid-beta binding
RT alcohol dehydrogenase (ABAD).";
RL J. Mol. Biol. 303:311-327(2000).

CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) -> 3-oxoacyl-CoA + NADH.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SCR) FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; AF049878; AAC05747.1; -
DR EMBL; AF069770; AAF14853.1; -
DR PDB; 1E3W; 25-MAY-01.
DR PDB; 1E3S; 25-MAY-01.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KM Oxidoreductase; NAD; Acetylation; 3D-structure.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT NP_BIND 11 36 NAD (BY SIMILARITY).
FT ACT_SITE 167 167 BY SIMILARITY.
FT CONFLICT 4 4 V -> C (IN REF. 2).
SQ SEQUENCE 260 AA; 27114 MW; 30F7E723A95F9227 CRC64;

Query Match 87.9%; Score 1151; DB 1; Length 260;
Best Local Similarity 87.7%; Pred. No. 1,8e-82;
Matches 228; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

QY 2 MAACRSYKGLVAVITGGASGLGATAEKLYGGASAVLLDLPNSGGEAOKKLGNNCYF 61
DB 1 MAACRSYKGLVAVITGGASGLGATAEKLYGGASAVLLDLPNSGGEAOKKLGNNCYF 60
QY 62 PAVTSEKDYQVATLALAKGFGVDVAVNCAGIAVASKTYNKKGQTHLEDFORVLDV 121
DB 62 PAVTSEKDYQVATLALAKGFGVDVAVNCAGIAVASKTYNKKGQTHLEDFORVLDV 120
QY 61 PAVTSEKDYQVATLALAKGFGVDVAVNCAGIAVASKTYNKKGQTHLEDFORVLDV 120
DB 61 PAVTSEKDYQVATLALAKGFGVDVAVNCAGIAVASKTYNKKGQTHLEDFORVLDV 120
QY 122 LMGTFTNIVIRIVAGEMQNEPDGQGGQGVITINTASVAFEGOVQAAYSASKGIYGMTL 181
DB 122 LMGTFTNIVIRIVAGEMQNEPDGQGGQGVITINTASVAFEGOVQAAYSASKGIYGMTL 180
QY 121 LIGTFNIVIRIVAGEMQNEPDGQGGQGVITINTASVAFEGOVQAAYSASKGIYGMTL 180
DB 121 LIGTFNIVIRIVAGEMQNEPDGQGGQGVITINTASVAFEGOVQAAYSASKGIYGMTL 180
QY 182 IARDLPIGIRVMTIAPGLTSLPEKYNFLASQVPPFSRLGDPAEVAHLVQAI 241
DB 182 IARDLPIGIRVMTIAPGLTSLPEKYNFLASQVPPFSRLGDPAEVAHLVQAI 240
QY 181 IARDLPIGIRVMTIAPGLTSLPEKYNFLASQVPPFSRLGDPAEVAHLVQAI 240
DB 181 IARDLPIGIRVMTIAPGLTSLPEKYNFLASQVPPFSRLGDPAEVAHLVQAI 240
QY 242 ENPFLNGEIVIRLDGAIKMP 261
DB 242 ENPFLNGEIVIRLDGAIKMP 260

RESULT 4
HCD2_MOUSE
ID HCD2_MOUSE STANDARD; PRT; 261 AA.

AC 008756;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)
DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein).
GN HADH2 OR HSD17B10 OR ERAB.
OS Mus musculus (Mouse).

```

HCD2_HUMAN          STANDARD;          PRT;          261 AA.
ID   HCD2_HUMAN
AC   O99714;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)
DE   (Endoplasmic reticulum-associated amyloid beta-peptide binding
DE   protein) (Short-chain type dehydrogenase/reductase XH9862).
GN   HADH2 OR ERAB OR XH9862 OR SCHAD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97478528; PubMed=9338779;
RA   Yan S.D., Fu J., Soto C., Chen X., Zhu H., Al-Mohanna F.,
RA   Collinson K., Zhu A., Stern E., Saigo T., Toyama M., Ogawa S.,
RA   Rohrer A., Stern D.;
RT   "An intracellular protein that binds amyloid-beta peptide and
RT   mediates neurotoxicity in Alzheimer's disease.";
RL   Nature 389:689-695(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Zhuchenko O.P., Wehnert M., Bailey J., Sun Z.S., Lee C.C.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96833780; PubMed=9671743;
RA   Miller A.P., Willard H.F.;
RT   "Chromosomal basis of X chromosome inactivation: Identification of a
RT   multigene domain in Xp11.21-p11.22 that escapes X inactivation.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:8709-8714(1998).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98221216; PubMed=9553139;
RA   He X.Y., Schuit H., Yang S.Y.;
RT   "A human brain L-3-hydroxyacyl-coenzyme A dehydrogenase is identical
RT   to an amyloid beta-peptide binding protein involved in Alzheimer's
RT   disease.";
RL   J. Biol. Chem. 273:10741-10746(1998).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RT   Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC   - FUNCTION: BINDS INTRACELLULAR AMYLOID-BETA. BY INTERACTING WITH
CC   AMYLOID-BETA, IT MAY CONTRIBUTE TO THE NEURONAL DYSFUNCTION
CC   ASSOCIATED WITH ALZHEIMER DISEASE.
CC   - CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
CC   + NADH.
CC   - SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC   - TISSUE SPECIFICITY: EXPRESSED IN NORMAL TISSUES BUT IS
CC   OVEREXRESSED IN NEURONS AFFECTED IN AD.
CC   - SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC   (SDR) FAMILY.
CC   -----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC   or send an email to license@sdb.ch).
CC   -----
EMBL: U96132; AAC51812.1; -
EMBL: U73514; AA868958.1; -
EMBL: AF068134; AAC39900.1; -
EMBL: AF035353; AAC15902.1; -

```

```

DR   EMBL: BC000372; AAH00372.1; -.
DR   HSSP; O70351; 1E3S.
DR   Genew; HGNC:4800; HADH2.
DR   MIM; 300256; -.
DR   InterPro; IPR002198; ADH_short.
DR   Pfam; PR00106; adh_short; 1.
DR   PRINTS; PR00080; SDRFAMILY.
DR   PROSITE; PS00061; ADH_SHORT; 1.
KW   Oxidoreductase; NAD.
FT   NP_BIND   12       37       NAD (BY SIMILARITY).
FT   ACT_SITE  168      168
FT   SEQUENCE  261 AA; 26923 MW; 9E74F242E3E6EF1 CRC64;
SQ
Query Match          100.0%; Score 1309; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 9.8e-95;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 MAACRSYVGLVAVITGASGLATAEERLVGQASAVLLDIPNSGGEAARKLNQVF 60
QY   1 MAACRSYVGLVAVITGASGLATAEERLVGQASAVLLDIPNSGGEAARKLNQVF 60
DB   1 MAACRSYVGLVAVITGASGLATAEERLVGQASAVLLDIPNSGGEAARKLNQVF 60
QY   61 APADVTSEKDVQALALAKGKGRVAVYAVNCAGIAVASTYMLKKGQTHLEDFQVLDV 120
QY   61 APADVTSEKDVQALALAKGKGRVAVYAVNCAGIAVASTYMLKKGQTHLEDFQVLDV 120
DB   61 APADVTSEKDVQALALAKGKGRVAVYAVNCAGIAVASTYMLKKGQTHLEDFQVLDV 120
QY   121 NLNGTFNVIRLVAGENGQNEPDGQGVYINTASVALEGGVGAAYSAKGIYGMTL 180
QY   121 NLNGTFNVIRLVAGENGQNEPDGQGVYINTASVALEGGVGAAYSAKGIYGMTL 180
DB   121 NLNGTFNVIRLVAGENGQNEPDGQGVYINTASVALEGGVGAAYSAKGIYGMTL 180
QY   181 PIARDLAPIGIRMTAPGIFGTPLLTSLPEKVCNLFASQVPPSLGDPAREYHLYQAI 240
QY   181 PIARDLAPIGIRMTAPGIFGTPLLTSLPEKVCNLFASQVPPSLGDPAREYHLYQAI 240
DB   181 PIARDLAPIGIRMTAPGIFGTPLLTSLPEKVCNLFASQVPPSLGDPAREYHLYQAI 240
QY   241 IENPFLNGEYIRLDGAIIRMP 261
QY   241 IENPFLNGEYIRLDGAIIRMP 261
DB   241 IENPFLNGEYIRLDGAIIRMP 261

RESULT 2
ID   HCD2_BOVIN          STANDARD;          PRT;          261 AA.
AC   O02691;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH).
GN   HADH2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=97214648; PubMed=9061028;
RA   Furuta S., Kobayashi A., Miyazawa S., Hashimoto T.;
RT   "Cloning and expression of cDNA for a newly identified isozyme of
RT   bovine liver 3-hydroxyacyl-CoA dehydrogenase and its import into
RT   mitochondria.";
RL   Biochim. Biophys. Acta 1350:317-324(1997).
CC   - CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
CC   + NADH.
CC   - SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC   - SUBCELLULAR LOCATION: Mitochondrial.
CC   - SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC   (SDR) FAMILY.
CC   -----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 14:19:47 ; Search time 7.83333 Seconds
(without alignments)
1381.956 Million cell updates/sec

Title: US-09-931-186-8
Perfect score: 1309
Sequence: 1 MAACRSVKGLVAVITGGAS.....ENPPLNGEVIIRLDGAIKMP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1309	100.0	261	1	HCD2_HUMAN
2	1206	92.1	261	1	HCD2_BOVIN
3	1151	87.9	260	1	HCD2_RAT
4	1132	86.5	261	1	HCD2_MOUSE
5	908	69.4	255	1	HCD2_PROMY
6	383.5	29.3	247	1	YD50_MYCTU
7	341	26.1	246	1	FABG_THEMA
8	334	25.5	320	1	FABG_CUPHA
9	332.5	25.4	261	1	DHBB_HUMAN
10	328.5	25.1	244	1	FABG_VIBCH
11	313.5	23.9	247	1	FAGI_SYNY3
12	313.5	23.9	260	1	DHBB_MOUSE
13	309.5	23.6	246	1	FABG_BACSU
14	305	23.0	260	1	YK02_MYCTU
15	301	23.0	255	1	YHFD_BACSU
16	299	22.8	255	1	2BHD_STRPX
17	294.5	22.5	248	1	Y4V1_RHISN
18	292	22.3	249	1	BAV1_EHBSB
19	291.5	22.3	244	1	FABG_VIBHA
20	290.5	22.2	248	1	FABG_AOUAE
21	289.5	22.0	244	1	FABG_ECOLI
22	288	22.0	263	1	UCPA_SALTY
23	287.5	22.0	246	1	PHBB_ALCEU
24	286	21.8	248	1	PHAB_ACTSP
25	284.5	21.7	256	1	Y019_THEMA
26	283.5	21.7	244	1	FABG_SALTY
27	281.5	21.5	246	1	NODG_AZOB
28	280	21.4	259	1	CMTB_PSEPU
29	279.5	21.4	241	1	PHBB_ZOORA
30	278.5	21.4	246	1	FABG_CHLMU
31	277.5	21.2	289	1	YHDF_BACSU
32	277	21.2	250	1	LINC_PSEPA
34	276	21.1	263	1	UCPA_ECO57
35	276	21.1	263	1	UCPA_ECOLI
36	275	21.0	246	1	PHBB_CHRVI
37	272	20.8	250	1	LINC_PSEPA
38	272	20.8	251	1	Y325_THEMA
39	272	20.8	319	1	FABG_ARATH
40	270.5	20.7	240	1	FABG_SYNY3
41	270.5	20.7	247	1	FABG_CHLTR
42	269.5	20.6	241	1	DHKB_STRCK
43	268.5	20.5	262	1	DHGB_BACME
44	267.5	20.4	336	1	TS2_MAIZE
45	266.5	20.4	241	1	PHBB_RHIME
46	266.5	20.4	242	1	FABG_HAEIN
47	264	20.2	247	1	FABG_MYCTU
48	261	19.9	261	1	DHG3_BACME
49	259	19.8	258	1	DHG2_BACSU
50	259	19.8	261	1	DHG3_BACME
51	259	19.8	261	1	DHG3_BACME
52	258	19.7	261	1	DHG2_BACME
53	257.5	19.7	238	1	Y0XD_BACSU
54	257	19.6	256	1	BUDC_KLEPN
55	257	19.6	261	1	DHG4_BACME
56	256	19.6	261	1	DHG1_BACME
57	254.5	19.4	241	1	FABG_RICPR
58	254	19.4	261	1	FABG_BACSU
59	251.5	19.2	267	1	SORD_KLEPN
60	250.5	19.1	266	1	PGDH_HUMAN
61	250.5	19.1	285	1	YHXC_BACSU
62	250	19.1	253	1	YAMP_RHISN
63	246.5	18.8	261	1	ACT3_STRCO
64	245.5	18.8	253	1	3BHD_CONTE
65	245	18.7	255	1	YV06_PSEAE
66	245	18.7	255	1	GNO_GLIOX
67	244.5	18.7	245	1	NODG_RHIS3
68	244.5	18.7	262	1	YXBG_BACSU
69	243	18.6	270	1	DHMA_FIASI
70	241.5	18.4	258	1	BDHA_RHIME
71	239	18.3	255	1	HDHA_ECOLI
72	238	18.2	247	1	FABG_PSEAE
73	238	18.2	255	1	FABG_MYCAV
74	237.5	18.1	261	1	YGCW_ECOLI
75	237	18.0	248	1	FABG_CHLPN
76	235	18.0	257	1	YXJF_BACSU
77	229.5	17.5	245	1	NODG_RHIME
78	229	17.5	894	1	FOX2_NEUCR
79	227.5	17.4	258	1	BDHA_ALCEU
80	226.5	17.3	242	1	PHAB_PARDE
81	226.5	17.3	273	1	TRN1_DAIET
82	224.5	17.2	249	1	DHKS_STRVN
83	224.5	17.2	256	1	DHKS_STRVN
84	224	17.1	254	1	IDNO_ECOLI
85	223.5	17.1	241	1	BUDC_KLEPE
86	222.5	17.0	256	1	MTDH_UREPA
87	222.5	17.0	900	1	FOX2_YEAST
88	222	17.0	255	1	FABG_MYCSM
89	221.5	16.9	285	1	GS39_BACSU
90	220.5	16.8	272	1	DHKL_STRVN
91	219.5	16.8	259	1	SLRD_ECOLI
92	219	16.6	248	1	Y452_LISIN
93	217	16.6	254	1	KDOD_BACSU
94	216.5	16.5	253	1	KDOD_ECOLI
95	216.5	16.4	242	1	FABG_ACTAC
96	213	16.3	134	1	DHBB_CALTA
97	212.5	16.2	248	1	Y432_LISMO
98	212	16.2	281	1	BPHB_COMTE
99	212	16.2	289	1	YHFD_BACSU
100	211.5	16.2	278	1	Y4V1_RHISN
08xpj4	escherichia				
P37440	escherichia				
P43575	chromatium				
P50198	pseudomonas				
Q9xyg0	thermocoga				
P33207	arabidopsis				
P73826	synecocyst				
P38604	chlamydia t				
P41177	streptomyces				
P07999	bacillus me				
P50160	zea mays (m				
P50205	rhizobium m				
P43713	haemophilus				
O48930	mycobacteri				
P10528	bacillus me				
P80869	bacillus me				
P39484	bacillus me				
P40988	bacillus me				
P39483	bacillus me				
P14802	bacillus su				
O48436	klebsiella				
P39485	bacillus me				
P39482	bacillus me				
P50941	rickettsia				
P12310	bacillus su				
P37079	klebsiella				
P15428	homo sapien				
P40397	bacillus su				
P55575	rhizobium s				
P16874	streptomyces				
P19871	comamonas t				
Q15176	pseudomonas				
P50199	gluconobact				
P27332	rhizobium s				
P46331	bacillus su				
P22441	flavobacter				
O86034	rhizobium m				
P25529	escherichia				
O54428	pseudomonas				
O07359	mycobacteri				
P76633	escherichia				
Q92892	chlamydia p				
P42317	bacillus su				
P06234	rhizobium m				
O01373	neurospora				
Q9x602	alcaligenes				
P02004	paracoccus				
P50162	datura stra				
P16543	streptomyces				
O59787	rhodobacter				
P39345	escherichia				
O04520	klebsiella				
O00058	ureomycetes fa				
Q02207	sebacaromyces				
P71533	mycobacteri				
P80873	bacillus su				
P16542	streptomyces				
P05707	escherichia				
O92977	listeria in				
P50842	bacillus su				
P37769	escherichia				
P70720	actinobacil				
O92963	callithrix				
P25145	listeria mo				
O46381	c cis-2,3-d				
P40398	bacillus su				
P55541	rhizobium s				

ALIGNMENTS

Thu Jun 26 06:55:12 2003

us-09-931-186-8.rspt

Page 12

DE 3'-oxoacyl-(acyl-carrier protein) reductase (EC 1.1.1.100).
GN FMBG OR BH2491.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132.
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kihara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RT Nucleic Acids Res. 28:4317-4331(2000).
CC 1- SIMILARITY. BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR FAMILY.
DR EMBL, AF001515, BAB06210.1, -.
DR HSSP, P19992, 1HDC.
DR InterPro, IPR002198, ADH_short.
DR Pfam, PF00106, adh_short, 1.
DR PRINTS, PRC0080, SDRFAMILY.
DR PROSITE, PS00061, ADH_SHORT, UNKNOWN_1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 246 AA; 26126 MW; 852B95EBBD9E950 CRC64;

Query Match	25.5%;	Score 333.5;	DB 16;	Length 246;
Best Local Similarity	34.2%;	Pred. No. 1.1e-15;		
Matches	90;	Conservative 42;	Mismatches 102;	Indels 29;
			Gaps	7;

QY	8	VKELVAVITIGGASGLTIAERLVGGASAVLTLDIPNSGCE-----	AOAKLGNVCV	59
Db	2	LOGKTAIVTGASGICRATAMELARHGAVVV-----	NYAGNKEKAKEKVAIVKRLGYEAL	57
QY	60	FAPADVTSERDVOGTALALAKGKEGRDVAVNCAGIAVASKITNYNKKGGTHTDEDFOVLD		119
Db	58	AICADVADSBSVQAMVKETIDTFEGAVDLIVNAGITRDNLEMRKE-----	EDMDAVID	111
QY	120	VNLMGFNYTRIVAGSMGONEBDOGOR-GVLIINASVAAPEGVQGAASASGCIYGM		178
Db	112	TNLKGFPHCKAKVTRPMKM-----	QREGRIINSSVYVGAIGNAGQANYAAAGVITGL	164
QY	179	TLEIADLAPIGIRVWTIAPGLGFPILTSLPEKCNCLASQVPEPSPGLDPATYAHVQ		238
Db	165	TKTLARLAKRNLTIVNAVAPGFTIEDMDIGELPEDEVKAOMLQDIFL-ARLGOPEEVAKAVR		223
QY	239	AIIEEN--PPLNGEIVFLDCAIRKM		259
Db	224	FLASDDASVLTGOTIEVNGGMV		246

Search completed: June 23, 2003, 14:32:47
Job time : 33.6667 secs

QY 128 VIRLYAAGEBQNEPPOGGRCVITINTASVAFEEQVYGAAASARSGIVGWTLPIDARDL 167
::: :|: |:
Db 121 VIKFSASKYMIK-----RKRIITISSVGLMGVGANTAAAKAGITIGTSSVAEELA 174
188 PIGIRMTLAPGLEFGPLTLSPKVCNFIASOVFFSRLDPAEVAHLYO--AIINPF 245
QY 175 SRGIYNANNAFPGIETDMTNVLKEDIKEAMLSIFL-KRAKPEBEVAEVAFILASSADY 233
::: ||: ||: |:
QY 246 INGEVIRILDGAIRM 259
:|: |: |: |:
Db 234 ITGQVINDDGAYM 247

RESULT 23	
042774	
ID 042774	PRELIMINARY; PRT; 297 AA

01-JUN-1998 (TREMBLrel. 06, Created)
 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 3-oxoacyl-[acyl-carrier-protein]-reductase.
 OAR_1 OR B2A19.180.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Sordariales; Sordariaceae; Neurospora.
 NCBI_TaxID=5141;
 [1]
 RP SEQUENCE FROM N.A.
 RA Buerger F., Brors B., Weiss H.;
 RL submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Algin V., Hobeisel J., Brandt P., Fartmann B., Holland R.,
 RA Mykatura G., Meves H.W., Mannhaupt G.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 DR EMBL: AF042860; AAB99739.1; -
 DR EMBL: AF039092; CAB98248.1; -
 DR HSSP: O70351.1; E6W.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 297 AA: 31342 MW; 8DC08FEDE5841966 CRC64;

Query Match	25.6%	Score 335.5	DB 3	Length 297
Best Local Similarity	31.7%	Pred. No. 1e-15		
Matches 97	Conservative 39	Mismatches 103	Indels 67	Gaps 8

```

QY      0  RESVKGLVAVITTGASGLGATARELVYGGQSAVLLDLPNS-----GGEAQ  50
      1  | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db      2  RSLIHQAOLITGGSGSIGLAIRRLYLEGCSVTLTGRESTEIORAQSLISQPLMSPAQ  61

QY      51  AKKLGNCCVAPADVTSEKDVQTAI-ALAKGKEGRVDVAVNCAGIAVAS---KTYNLKKG  106
      6  | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db      62  QPSDRKRVSYHPLNVAISASMEDLLQNSNKGKGRVDILINCAGITQRPSELMKT-----  115

QY      107  QHTLEDFFQRYLDVNLKGFNFVIRLYAAGEGQNEP-----DDGG-----  145
      1  | : | : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      116  ---SIEVEGLDLDTNLRGTVLGCKFPGRALIRRRPQQOHPRYKADSEGAEGVEGTEEG  172

QY      146  -----ORGVIINTASVAAFEGOVQQAASAKSGKGIWGLTEIARDLAFGI  191
      1  | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      173  KEGSKGQGVREGVQGERVGIINVASLLAQKRVIGTSYAAAKACAGVGLTSLAHBYGRSGI  223

QY      192  RWVTIAPGLTGFTLLSLPEKVCNFTASQVPPDSRLCDPAEIAHLVAOAITENPFLNCEVI  25

```

D6	233	RVAAVLDGTYETDMDTGLKNP---	SILQCIPL-GFGITDEVADAALFLINPNANNCVL	288
OY	252	RLDGAI	257	
Db	289	NLDGGL	294	

RESULT 24	
Q8YVT0	
ID Q8YVT0	PRELIMINARY; PRT; 251 AA

```

DT      01-MAR-2002 (TREMBLrel. 20 Created)
DT      01-MAR-2002 (TREMBLrel. 20, last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE      3-oxoacyl-l-acyl-carrier protein) reductase.
GN      FABG OR ALR1894.
OS      Anabaena sp. (strain PCC 7120).
OC      Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX      NCBI_TaxId=103690;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21595285; PubMed=11759840;
RA      Kaneo T., Nakamura Y., Wolk C.P., Kunitz T., Sasamoto S.,
RA      Watanabe A., Iizuguchi M., Ishikawa A., Kawashima K., Kimura T
RA      Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA      Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA      Yasuda M., Tabata S.;
RT      *complete genomic sequence of the filamentous nitrogen-fixing
RT      cyanobacterium Anabaena sp. strain PCC 7120."
RL      DNA Res. 8:205-213(2001).
RL      EMBL; AP003587; BA573593.1; -.
DR      InterPro; IPR002198; ADH_short.
DR      InterPro; IPR001092; HLH_basic.
DR      Pfam; PF00106; adh_short; 1.
DR      PRINTS; PR00080; SDRFAMILY.
DR      PROSITE; PS00065; ADH_SHORT; 1.
DR      PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN.1.
SQ      complete proteome.
SQ      SEQUENCE 251 AA; 26218 MW; 57D0712FE8AB698 CRC64;

```

Query Match	25.6%;	Score 334.5;	DB 16;	Length 251;
Best Local Similarity	33.1%;	Pred. No. 1e-15;		
Matches 91; Conservative	46;	Mismatches 97;	Indels 41;	Gaps 7.

```

QY      MAACSGSVGLVITGGAGSGGLAAERIVYGGA-----VLIDLEPNSG 47
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 MALLSENIRGQAVVYVIGASRGISRAIATELANYGATVYVNVYASSPAADEVAEITGAG 60

QY      48 EAQAKTLGNCCVAPADVYSEKDYQNALAKSPERVAVYAVACIAVASKTYNLRKG 107
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61 EAVALK-----ADVSGVEQVDNLINAIKFKRIDLVYNNAGITROTLLREKP-- 109

QY      108 THRLDEQRYLVYLMGTEVITPLVYCEQGNPEPDGGQGVYIINTASVAFEGVQGOA 167
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 ----EMQAVITDNLGVFLCTRAVSLMKQ-----RSGRITINTSVAGQGNQGAN 159

QY      168 YSASKGIVGMPLPIARDLAPICIRVYTAGLFGTPLTSLPEKVCNFIASVQPPPSRL 227
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      160 YSAAKGVGISTFTYVAEILASRGITVYNAVAPGGLIADMISNLSKSE--GILQYIPL-GRY 215

QY      228 GDPAEYAHLYQATIENP--FLNGEVIRLDGAIRM 259

Db      216 GQPEIRIGVRYFLAADPAAVYITGVYVNDGGVM 250

```

RESULT	25	
Q9KRA03		
Q9KRA03	PRELIMINARY;	PRT; 246 AA.
AC Q9KRA03		
DT 01-OCT-2000	(TEMPREL.. 15,	Created
DT 01-OCT-2000	(TEMPREL.. 15,	Last sequence update)
DT 01-JUN-2002	(TEMPREL.. 21,	Last annotation update)

Thu Jun 26 06:55:12 2003

us-09-931-186-8.rspc

Page 9

DB 8 AVITGXXXXXKAGGAPRRRL---ARSALFDLNDKGAAGVAGIGADKARYFNVNS 63
QY 67 SEKDVQALALAKGKFRVDVAVNCAGIAVASKTYNKKQOTLLEDFQVLDVNLMTGTE 126
DB 64 DEAAVTAIDQAHDFLEGLGLVAVNMCAGIILGAGRY--LGKRGPMPLAGFGGTAVVNLVGSF 121
QY 127 NVIRLVAGEMGQNPDDGGQGVIIINTASVAAPFEGVGAAYASKSGIYGMPLIARDL 186
DB 122 NVAKAANRMQHNAGTGERGVYIINTASIAAYEGIGGAAYASKSGVSMPLPMAREL 181
QY 187 APIGIRVATLAPGLFGLTSLPEKY 213
DB 182 SRFGRVNTIAPGVFWPMDGMEAV 208

RESULT 18

Q8XHL1 PRELIMINARY; PRT; 246 AA.
AC 08XHL1.
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 3-oxoacyl-[acyl-carrier-protein] reductase.
GN FABG OR CPE1070.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / TYPE A;
RX PubMed=11792842;
RA Shintzu T., Ohtani K., Hirakawa H., Oshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AP003189; BAB8076.1; -
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KM Complete proteome.
SQ SEQUENCE 246 AA; 26267 MW; CD90B6C650ECC817 CRC64;

Query Match 28.5%; Score 373.5; DB 16; Length 246;
Best Local Similarity 35.8%; Pred. No. 1.9e-18;
Matches 93; Conservative 47; Mismatches 97; Indels 23; Gaps 7;

QY 8 VGVIAVITGASGLGATAEKRLVGGASAVLDDPNSGGEQAARKL-----GNCCVAP 62
DB 2 LDKDAVIAVITGGRIGRATLALADOGAN-IVINRNSDKAEELKALIEEKGVIVTK 60
QY 63 ADVTSKDVQALALAKGKFRVDVAVNCAGIAVASKTYNKKQOTLLEDFQVLDVNL 122
DB 61 CQISNEDSKNLMDCKEVEFKIDILVNNAGITKTLIRKRE-----EDDNVLDVNL 114
QY 123 MGTENVIRLVAGEMQNPDDGGQGVIIINTASVAAPFEGVGAAYASKSGIYGMPL 181
DB 115 KGTENCAKHAISIMK-----QRFKILNMTSVVGINAGVYASKSGIYGLTKS 167
QY 182 IARDLAPIGIRVATLAPGLFGLTSLPEKYCNFLASQVPPSPRLGDPAEVAHLVQAL 241
DB 168 LAKELGSRGITVAVNAPGFIINDMTASLEKYEKESKNIPL-KRLGDEVDVAVNLVGSF 226
QY 242 ENP--FLNGEYIRLDGAIK 259
DB 227 SDANVITGVIVNDGMVA 246

RESULT 19
Q99YD6 PRELIMINARY; PRT; 244 AA.
ID Q99YD6

AC Q99YD6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative beta-ketacyl-ACP reductase (EC 1.1.1.100).
GN FABG OR SPY1749.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP370 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin K.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AE006603; AAK34493.1; -
DR HSP; P50162; IAE1.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR01608; BACINVASINC.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00036; HELIX_LOOP_HELIX; UNKNOWN_1.
KM Oxidoreductase; Complete proteome.
SQ SEQUENCE 244 AA; 26002 MW; 67ECE23670D40D65 CRC64;

Query Match 27.2%; Score 355.5; DB 16; Length 244;
Best Local Similarity 35.4%; Pred. No. 3.4e-17;
Matches 92; Conservative 41; Mismatches 102; Indels 25; Gaps 5;

QY 8 VGVIAVITGASGLGATAEKRLVGGASAVLDDPNSGGEQAARKL-----GNCCVAP 60
DB 3 IKGRNIRITGSTRIGIGAMAHQFASLEAVTL-----NGSASSEELVASTDYGVVY 57
QY 61 APADVSEKDVQALALAKGKFRVDVAVNCAGIAVASKTYNKKQOTLLEDFQVLDV 120
DB 58 ISGVDSASAEKKRVNVAISLSIGSIDVAVNNAGIT-----NDKIMLKTEEDFERVTK 111
QY 121 NMGTEFVIRLVAGEMQNPDDGGQGVIIINTASVAAPFEGVGAAYASKSGIYGMPL 180
DB 112 NLGAFNMGTQSVL-----KPMIKARQALINSSVGLTGNIGQAVYASKSGIYGLTK 165
QY 181 PIARDLAPIGIRVATLAPGLFGLTSLPEKYCNFLASQVPPSPRLGDPAEVAHLVQAL 240
DB 166 SVAREVAARNICVAVNAPGFIESDMTGVLPKMEQLLSQPM-KRLGKQOVAHLASFL 224
QY 241 IENPFLNGEYIRLDGAIK 260
DB 225 VEODYITGVIVNDGMTQ 244

RESULT 20

Q9HW15 PRELIMINARY; PRT; 252 AA.
AC Q9HW15;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Probable short-chain dehydrogenase.
GN PA4389.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]

Thu Jun 26 06:55:12 2003

us-09-931-186-8.rspt

Page 8

ID 08T2L7 PRELIMINARY: PRT: 264 AA.
AC 08T2L7;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DB 3-hydroxyacyl-CoA dehydrogenase type II.
OS Dictyostellium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidia; Dictyostellium.
NCBI_TaxID=44689;
X [1]
RN SEQUENCE FROM N.A.
RP STRAIN=AX4;
RA Gloeckner G., Eichinger L., Szafarski K., Pachabati J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guido R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and Analysis of Chromosome 2 of Dictyostellium.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC115594; AAL92306.1; -
SQ SEQUENCE 264 AA; 28795 MW; 3C0007DA1309F294 CRC64;
Query Match 46.1%; Score 603.5; DB 5; Length 264;
Best Local Similarity 48.8%; Pred. No. 2,6e-34;
Matches 127; Conservative 46; Mismatches 78; Indels 9; Gaps 5;
QY 8 VKGLVAVITGASGLGATLAEKLVGOGASAVLDDLPNSGGEAOKKLGNNCFAPADVTSEKD 66
DB 3 INGTFFVVTGGASGLGLETSHRLSGANIFIMDMNEENGRKYVEELGSKTFESSVDIT 62
QY 67 SEXVOYALALAKKPKFQVAVNACAGIAVASKYNNLKKGOTLLEDFQVLDVNLNGTF 126
DB 63 LEDSVKSLSEHCKLKEFHEHGVINAGVAAAGVRIK RDGQVHPLDFTVAVVNLIGTF 121
QY 127 NVIRLVAGEM-GONEPD--OGG---QGVYIINTASVAFAEGVGOAGVYASAGGIVGNT 179
DB 122 NVIRLVADIDHNOQPSKDGEEEEKGVFIMTASVAFAEGVGOAGVYASAGGIVGNT 181
QY 180 LPIRADLAPIGIRMTIAPGLFTPLTSLPEKCNFLASOVPPSRIGDPAEYAHLYQA 239
DB 182 LPMAREFTLTKIRINTIAPGFTETPVMELPQAIKINSIESIPPSMGKPKERAFILQCH 241
QY 240 IIEENFLNGEYIRLDGAIRM 259
DB 242 LIENYINGEYIRLDGALRL 261
RESULT 16
Q9ABU6 PRELIMINARY: PRT: 260 AA.
AC Q9ABU6;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DB 3-hydroxyacyl-CoA dehydrogenase.
CC0124.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
NCBI_TaxID=155892;
X [1]
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC 19089 / CB15;
RA MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohia N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA Debey R.T., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouli H., Shetty J., Berry K.,
RA Ueberback S.L., Venter J.C., Shapiro L., Fraser C.M.;
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY

DR EMBL: AE005687; AAK22111.1; -
DR HSSP: 070351; IE3S.
DR TIGR: CC0124; -
DR InterPro: IPR002198; ADH_short.
DR InterPro: IPR002025; NAD_binding.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 260 AA; 27075 MW; 7DC145D069C89029 CRC64;
Query Match 45.5%; Score 595; DB 16; Length 260;
Best Local Similarity 51.0%; Pred. No. 9,8e-34;
Matches 130; Conservative 30; Mismatches 89; Indels 6; Gaps 2;
QY 11 LVAVITGASGLGATLAEKLVGOGASAVLDDLPNSGGEAOKKLGNNCFAPADVTSEKD 70
DB 7 VAAVITGASGLGATLAEKLVGOGASAVLDDLPNSGGEAOKKLGNNCFAPADVTSEKD 64
QY 71 VQALALAKKFKGRVDVAVNACAGIAVASKYNNLKKGQVHT----LEDFQVLDVNLNGTF 126
DB 65 VDAGEFKRRAAGQERILVNCAGTGNARKTASRDATGETVHFPLDADRILQINLVGTF 124
QY 127 NVIRLVAGEMGONEDDGGGSGVINTASVAFAEGVGOAGVYASAGGIVGNTLPIARDL 186
DB 125 RCIASAKGMDDLEFLDEGERALVNTASVAFAEGVGOAGVYASAGGIVGNTLPIARDL 184
QY 187 APIGRVMTIAPGLFTPLTSLPEKCNFLASQVPPFSRLGDPAEYAHLYQAIIENPFL 246
DB 185 MGEGRVNTILPGIFNTPLMNNAPPAVYAGLAASVFPFRLGHPREYAOALATMTTCGF 244
QY 247 NGEVIRLDGAIRM 261
DB 245 NGEVDVLDGIRNAP 259
RESULT 17
Q93SJ3 PRELIMINARY: PRT: 443 AA.
AC Q93SJ3;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DB USCS-2P.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
OC Myxococcales; Cystobacteriineae; Myxococcaceae; Myxococcus.
NCBI_TaxID=34;
X [1]
RN SEQUENCE FROM N.A.
RP STRAIN=CECT 422;
RA Poza M., Siefert C., Villa T.G.;
RT "Clone USCS from Myxococcus xanthus CECT 422 strain.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
CC EMBL: AY033405; AAK49009.1; -
DR InterPro: IPR002198; ADH_short.
DR InterPro: IPR001059; EF-P.
DR InterPro: IPR001092; HLH_basic.
DR Pfam: PF00106; adh_short; 1.
DR Pfam: PF01132; BFP; 1.
DR PROSITE: PS00061; ADH_SHORT; UNKNOWN; 1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN; 1.
KW Oxidoreductase.
SQ SEQUENCE 443 AA; 47589 MW; 214157EDFD5F2A20 CRC64;
Query Match 29.5%; Score 386; DB 2; Length 443;
Best Local Similarity 46.4%; Pred. No. 5,3e-19;
Matches 96; Conservative 29; Mismatches 70; Indels 12; Gaps 5;
QY 13 AVITG---GASGLGATLAEKLVGOGASAVLDDLPNSGGEAOKKLGNNCFAPADVTSEKD 66
DB 13 AVITG---GASGLGATLAEKLVGOGASAVLDDLPNSGGEAOKKLGNNCFAPADVTSEKD 66

Db 187 MTIACGITEETPMACMTEEBRASLAVPPEPRLGRPOEYAAALARIHENSMTNGEYIRL 246
 Qy 254 DGAIRM 259
 Db 247 DGAIRM 252

RESULT 13

080F12 PRELIMINARY: PRT: 257 AA.

AC 080F12;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE 3-hydroxyacyl-CoA dehydrogenase type II.
 GN ATU1415 OR AGR_C_2613.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_Taxid=176299;
 RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-21608550; PubMed-11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D., St.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kitayvin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Seshphimachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krepan M., Perry J.,
 RA Gordon-Kamm B., Liao L., Kim S., Kendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT C58.";
 RL Science 294:2317-2323(2001).

RN [2]

RP SEQUENCE FROM N.A.
 RA MEDLINE-21608551; PubMed-11743194;
 RA Goodner B., Hinkle G., Gestung S., Miller N., Blanchard M.,
 RA Querillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmel K., Gordon J., Vaudin M., Tatchouk O., Epp A., Liu F.,
 RA Woliam C., Allinger M., Doughy D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328(2001).
 DR EMBL: AE009102; AAL42421.1;
 DR EMBL: AE008067; AAK87207.1;
 KW Complete proteome.
 SO SEQUENCE 257 AA; 26622 MW; FF74A61FEC4B2B5C CRC64;

Query Match 49.0%; Score 642; DB 16; Length 257;
 Best Local Similarity 51.7%; Pred. No. 5.4e-37;
 Matches 134; Conservative 41; Mismatches 76; Indels 8; Gaps 3;

Qy 7 SVKGLVAVITGGASGIGLTAERLVGQASAVLLDPLNSGGFAOKKIGNNCPAPADVT 66
 Db 2 NIEGAGALVTGAASGIGAAVVARMLAARGAATVIFPRNGEAGKRLAAEIGKAV--QGCVT 59
 Qy 67 SEKDVOGTALAKGKRGVDAVNAAGIVASKTYNLKGGTHTEDFORVLDVNLKGT 126
 Db 60 SDDDAARAKVAAASAGGRLILVNCAGITAGRT--LGRBGPRLGDEQVIRVNLITF 117
 Qy 127 NVIRLVAGMGQNEPDG---GQKGVITNTASVAAFEGQQAAYASAKGIGVMTLP 182
 Db 118 NMRRLAAAHAAERDEGDSRDNGVIVNTASVAAFEGQIQAAAYASAKGIGVSLADPA 177
 Qy 183 ARDLAPLIGIVMTIAGLFGTPLTSLPEKVCNPLASQVPPSRIGDAEVAHYVAIT 242
 Db 178 ARRLAFRIKRVNTVAGIIFLTPLLOGILPQEVESLAGEQIPHSRIGDPAERFADYRFLIE 237

Qy 243 NEPLNGEYIRLDGAIRMOP 261
 Db 238 NDYNGEYIRLDGAIRMOP 256

RESULT 14

09DCX5 PRELIMINARY: PRT: 126 AA.

AC 09DCX5;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Hydroxacyl-coenzyme A dehydrogenase, type II.
 GN HSD17B10 OR HADH2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikiado I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 RA Sakai K., Orligo T., Furuno M., Aono H., Baladevall R., Barsh G.,
 RA Blake J., Botfield D., Boujunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kanlaya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
 RA Suzuki H., Toyokura K., Wang K.H., Weltz C., Whitaker C., Wilmberg L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 DR EMBL: AK002368; BAB22046.1;
 DR HSSP: A70351; 1E6W.
 DR MGD: MGI:1333871; Hsd17b10.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Oxidoreductase.
 SO SEQUENCE 126 AA; 13265 MW; 78FFB6D441B9989D CRC64;

Query Match 46.4%; Score 607; DB 11; Length 126;
 Best Local Similarity 95.2%; Pred. No. 6.2e-35;
 Matches 120; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 136 MGNEDPDGQGRGVITNTASVAAFEGQQAAYASAKGIGVMTLPPIARDLAPIGIRYMT 195
 Db 1 MGNEDPDGQGRGVITNTASVAAFEGQQAAYASAKGIGVMTLPPIARDLAPIGIRYMT 60
 Qy 196 IARGLEGTPLTSLPEKVCNPLASQVPPSRIGDAEVAHYVAITNEPLNGEYIRLDG 255
 Db 61 IARGLEGTPLTSLPEKVCNPLASQVPPSRIGDAEVAHYVAITNEPLNGEYIRLDG 120
 Qy 256 AIRMOP 261
 Db 121 AIRMOP 126

RESULT 15
 0812L7

NCBI_TaxID=305;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-GM11000;
 RA MEDLINE-21681879; PubMed-11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Ariat M., Billault A., Brotlier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choisme N., Claudel-Renard C., Cunac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Siguler P., Thebaud P., Whalen M., Winkler P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*,"
 RL Nature 415:497-502(2002).
 DR EMBL; AL646070; CAD16241.1; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short.1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR Oxidoreductase; Complete proteome.
 SQ SEQUENCE 252 AA; 25642 MW; D6BEACDA99179DF CRC64;
 Query Match 52.7%; Score 689.5; DB 16; Length 252;
 Best local similarity 57.1%; Pred. No. 2,7e-40;
 Matches 145; Conservative 33; Mismatches 71; Indels 5; Gaps 3;
 QY 8 VKGLAVITGASGLGATLAEELVGGASAVLDDLPSNGGEAOKKLGNNCVFAPADYTS 67
 Db 3 IRDQVEIYTGASGIGAGITPRALAEAGKVVADLNAGAAAOEIGGR--FVRCVSS 60
 QY 68 EKDQOTALAKKGFGRVDVAVNCAGTAVASKTYNLKKGTHTEDEFORVLDVNLMTFN 127
 Db 61 EADGAAVQAAFT-SIGALAGLVNCAAGTAPASRT--VKGAGHPHLDQARAVINILIGTFN 117
 QY 128 VIRLVAGMGQNEPDGQGVIIINTASVAAFEGQVQAAVSASKSGITVGTLPDIADLA 187
 Db 118 MIRLAFATMTANAPAGGEGVITINTASVAAFDQIGQAAVYASKGVVAATLAIADLS 177
 QY 188 PIGIVMTIAGLGTPLTSLPERKVCNFLASQVPEPSRLGDPPEYAHVLAQIIEPNFLN 247
 Db 178 RDGIIVMTIAGLGTPLTSLPERKVCNFLASQVPEPSRLGDPPEYAHVLAQIIEPNFLN 237
 QY 248 GEVIRLDGAIRMOP 261
 Db 238 GETIRLDGAIRMOP 251
 RESULT 9
 ID 006544 PRELIMINARY; PRT; 250 AA.
 AC 006544;
 DT 01-JUL-1997 (TREMblrel. 04, Created)
 DT 01-JUL-1997 (TREMblrel. 20, last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, last annotation update)
 DE Oxidoreductase, short-chain dehydrogenase/reductase family.
 GN RV1144 OR MTC165.11 OR MT117.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriales; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA MEDLINE-98295987; PubMed-9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmler K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Baaham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holtroyd S.,
 RA Hornby T., Jorgels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream A.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of *Mycobacterium tuberculosis* from the
 complete genome sequence."

RL Nature 393:537-544(1998).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN-CDC 1551 / OSHKOSH;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and
 laboratory strains."
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; Z95584; CAB09032.1; -
 DR EMBL; AE006996; AAK45436.1; -
 DR HSSP; 070351; 1E3S.
 DR TIGR; MT1177; -
 DR Tuberculist; RV1144; -
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR00205; NAD-binding.
 DR Pfam; PF00106; adh_short.1.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR Hypothetical protein; Complete proteome.
 SQ SEQUENCE 250 AA; 25787 MW; 123A1005A12BD66 CRC64;
 Query Match 51.3%; Score 671.5; DB 16; Length 250;
 Best local similarity 60.1%; Pred. No. 4,7e-39;
 Matches 152; Conservative 25; Mismatches 69; Indels 7; Gaps 4;
 QY 9 KGLAVITGASGLGATLAEELVGGASAVLDDLPSNGGEAOKKLGNNCVFAPADYTS 68
 Db 4 KDAVAVTGGASGLGATLAEELVGGASAVLDDLPSNGGEAOKKLGNNCVFAPADYTS 60
 QY 69 KDQOTALAKKGFGRVDVAVNCAGTAVASKTYNLKKGTHTEDEFORVLDVNLMTFN 128
 Db 61 AAVSNALIELA-DSLGPVRYVYVNCAGTGNARV--LRDQVGPLAARKIYDILVGTFFV 117
 QY 129 IRLVAGMGQNEPDGQGVIIINTASVAAFEGQVQAAVSASKSGITVGTLPDIADLA 188
 Db 118 IRLGAEIRIAKTEP-IGERGVIINTASVAAFDQIGQAAVYASKGVVAATLAIADLS 176
 QY 189 IGIRVMTIAGLGTPLTSLPERKVCNFLASQVPEPSRLGDPPEYAHVLAQIIEPNFLN 248
 Db 177 KLIRVMTIAGLGTPLTSLPERKVCNFLASQVPEPSRLGDPPEYAHVLAQIIEPNFLN 236
 QY 249 EVIRLDGAIRMOP 261
 Db 237 EVIRLDGAIRMOP 249
 RESULT 10
 ID 092YS1 PRELIMINARY; PRT; 255 AA.
 AC 092YS1;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, last annotation update)
 DE Probable.
 GN RA0792 OR SMA1452.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Rhizobium pSymA (megaplasmid 1).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1021;
 RA MEDLINE-21396509; PubMed-11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
 RA Gurjani M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis K.W., Federspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire

OY 123 MGTENVIRLAVAGMONEPDGORGVIINTASVAEFGVGOAAYSASKGIVGMLPDI 182
 Db 120 LGTFNVRHGVALMGEHEKNDANGORGVIINTASVAEFGDGTGQSAYSASKGIVGMLPDI 179
 OY 183 ARDLAPGIRVMTAPGLFTGTPLLTSLPEKYCNFLASQVFPFRLDPAEYALVQALIE 242
 Db 180 ARDPAGGIRFNTTAPGLMDPTLLSLPEKVSFLAOLIPNPSRLGHPHFGALVQHILE 239
 OY 243 NPFLNGEVIKLDGAIRM 259
 Db 240 NGVINGETIRFDGALRM 256

RESULT 6

Q910T0 PRELIMINARY; PRT; 255 AA.
 AC 0910T0:
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Probable short-chain dehydrogenase.
 GN PA2554.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 RX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltz L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lam R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reiter U., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen."
 RT Nature 406:959-964(2000).
 CC -1. SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 CC EMBL: AE004683; AAG05942.1; -
 DR HSPF; C70351.1; 1B3S.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short.1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT.1.
 KW Oxidoreductase; Complete proteome.
 SO SEQUENCE 255 AA; 26426 MW; E8BF28712D2936D CRC64;

Query Match 55.0%; Score 720; DB 16; Length 255;
 Best Local Similarity 57.5%; Pred. No. 2,1e-42;
 Matches 145; Conservative 39; Mismatches 66; Indels 2; Gaps 1;

OY 8 VKGLAVITGASGLATAERLVGOGASAVLLDLPNSGGEQAOKLGNCCVFAPADVTS 67
 Db 3 IENRFVITGSGSGGLATAKLVGGGKVVLDINAEGAKAKELGAQAREVADIAS 62
 OY 68 EKDVOITALAKKGRGVDAVNCAGIAVASTYLLKKGGHTLEDFOVLDVNMGTEN 127
 Db 63 EADGRQVAAALAEAGLGLANLCAGVAPAEKV--LGRNGHALDSFRFVIDINLVGSFN 120
 OY 128 VIRLVAGEMONEPDGORGVIINTASVAEFGVGOAAYSASKGIVGMLPDIARDLA 187
 Db 121 MLRLAELMSQGPDEGSRGIVMTASAAFDGQIGAAIYASKSGVGMPLIARELA 180
 OY 188 PIGIRVMTAPGLFTGTPLLTSLPEKYCNFLASQVFPFRLDPAEYALVQALIEPFLN 247
 Db 181 RIGIRVMTAPGLFTGTPPMAGMFOEVODLIGASVFPFRLGEPAEYALVRAIIVNOMLN 240
 OY 248 GEVIRLDGAIRM 259
 Db 241 GEVIRLDGAIRM 252

RESULT 7

Q8YBSO PRELIMINARY; PRT; 255 AA.
 ID 08YBSO:
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE 3-oxoacyl-(acyl-carrier protein) reductase (EC 1.1.1.100).
 GN BMEI10816.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Brucellaceae; Brucella.
 RX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mujer C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykdis A., Reznik G.,
 RA Jablonksi L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyrides N., Overbeek R.,
 RA "The genome sequence of the facultative intracellular pathogen
 Brucella melitensis."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 RL EMBL: AE009715; AA154058.1; -
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short.1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT.1.
 KW Oxidoreductase; Complete proteome.
 SO SEQUENCE 255 AA; 26263 MW; 5CF61D4B37F6B730 CRC64;

Query Match 54.3%; Score 711; DB 16; Length 255;
 Best Local Similarity 57.1%; Pred. No. 9e-42;
 Matches 144; Conservative 37; Mismatches 69; Indels 2; Gaps 1;

OY 8 VKGLAVITGASGLATAERLVGOGASAVLLDLPNSGGEQAOKLGNCCVFAPADVTS 67
 Db 3 IENRFVITGSGSGGLATAKLVGGGKVVLDINAEGAKAKELGAQAREVADIAS 62
 OY 68 EKDVOITALAKKGRGVDAVNCAGIAVASTYLLKKGGHTLEDFOVLDVNMGTEN 127
 Db 63 DTGKAAITAAIAEFNSHIDVNCAGVAPBEKV--LGRGAHLLEFTTISINLIGTFN 120
 OY 128 VIRLVAGEMONEPDGORGVIINTASVAEFGVGOAAYSASKGIVGMLPDIARDLA 187
 Db 121 MLRLAELMSQGPDEGSRGIVMTASAAFDGQIGAAIYASKSGVGMPLIARELA 180
 OY 188 PIGIRVMTAPGLFTGTPLLTSLPEKYCNFLASQVFPFRLDPAEYALVQALIEPFLN 247
 Db 181 RIGIRVMTAPGLFTGTPPMAGMFOEVODLIGASVFPFRLGEPAEYALVRAIIVNOMLN 240
 OY 248 GEVIRLDGAIRM 259
 Db 241 GEVIRLDGAIRM 252

RESULT 8

Q8XWEO PRELIMINARY; PRT; 252 AA.
 ID 08XWEO:
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Probable 3-hydroxyacyl-CoA dehydrogenase type II oxidoreductase
 protein (EC 1.1.1.35).
 GN RSC2534 OR RS05766.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 CC Ralstonia.

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,
 RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guisticini S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbets P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Welter C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RA "Functional annotation of a full-length mouse cDNA collection.",
 RT Nature 409:685-690(2001)
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 DR EMBL: AK013340; BAB28800.1; -.
 DR HSSP: O70351; 1B6W.
 DR MGD: MGI:133871; Hsd17B10.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Oxidoreductase.
 SQ SEQUENCE 261 AA; 27273 MW; F36CD19GCFEEFAF CRC64;

Query Match 88.1%; Score 1153; DB 11; Length 261;
 Best Local Similarity 87.4%; Pred. No. 2.4e-72;
 Matches 228; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

OY 1 MAACRSYKGLAVITGASGLGATATRLVGGASAVLLDLPNSGGEAOKKGNVCV 60
 DB 1 MAASVSVKGLAVITGASGLGATATRLVGGASAVLLDLPNSGGEAOKKGNVCV 60
 OY 61 APADYSEKDVOTATLAKGKRGVAVNCGIYVASKTYNLKGGTHTLEDFORVLDV 120
 DB 61 APANTSKRELQALTLAKKEGGRIDVAVNCGIYVASKTYNLKGGTHTLEDFORVLDV 120
 OY 121 NMGTFNIVRLVAGMGONPDGQGRVYIINTASVAAFEGVGQAAVSASKGIVGML 180
 DB 121 NMGTFNIVRLVAGMGONPDGQGRVYIINTASVAAFEGVGQAAVSASKGIVGML 180
 OY 181 PIARLAPLIGIRVMTIAPGLFTPLTSLPEKVCNFTLSOYFEPRLDPAEYAHLYQAI 240
 DB 181 PIARLAPLIGIRVMTIAPGLFTPLTSLPEKVCNFTLSOYFEPRLDPAEYAHLYQAI 240
 OY 241 IENPFLNGEVIRLDGAIKMQP 261
 DB 241 IENPFLNGEVIRLDGAIKMQP 261
 RESULT 4
 ID 08TCV9 PRELIMINARY; PRT; 196 AA.
 AC 08TCV9;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Endoplasmic reticulum-associated amyloid beta peptide-binding protein
 DE (Fragment).
 GN ERAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Deininger M.H., Meyerman R., Schluesener H.J.;
 RT "Expression, release and induction of endoplasmic reticulum-associated
 RT amyloid beta-binding protein in brain disease."
 RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY092415; AAM18189.1; -.
 FT NON_TER 1 1
 FT NON_TER 196 196
 SQ SEQUENCE 196 AA; 20581 MW; 2400DE14966BAA6A CRC64;

Query Match 75.9%; Score 993; DB 4; Length 196;
 Best Local Similarity 100.0%; Pred. No. 2e-61;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 AKKLGNVCYFAPADYSEKDVOTATLAKGKRGVAVNCGIYVASKTYNLKGGTHT 110
 DB 1 AKKLGNVCYFAPADYSEKDVOTATLAKGKRGVAVNCGIYVASKTYNLKGGTHT 60
 OY 111 LEDFORVLDVNLGTFNIVRLVAGMGONPDGQGRVYIINTASVAAFEGVGQAAVSA 170
 DB 61 LEDFORVLDVNLGTFNIVRLVAGMGONPDGQGRVYIINTASVAAFEGVGQAAVSA 120
 OY 171 SKGGIVGMLPIARDLAPLIGIRVMTIAPGLFTPLTSLPEKVCNFTLSOYFEPRLD 230
 DB 121 SKGGIVGMLPIARDLAPLIGIRVMTIAPGLFTPLTSLPEKVCNFTLSOYFEPRLD 180
 OY 231 AEYAHLYQAIENPFL 246
 DB 181 AEYAHLYQAIENPFL 196

RESULT 5
 ID 019102 PRELIMINARY; PRT; 258 AA.
 AC 019102;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Probable 3-hydroxycyl-CoA dehydrogenase F0164.2 type II (EC 1.1.1.35)
 DE (Type II HADH).
 DE F0164.2.
 GN Caenorhabditis elegans.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peliorderinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Harris B.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: L-3-HYDROXYCYCL-COA + NAD(+) = 3-OXOCYCL-COA +
 CC NADH.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC FAMILY (SDR).
 CC EMBL: Z68341; CA92764.1; -.
 DR EMBL: Z68341; CA92764.1; -.
 DR HSSP: O70351; 1B6W.
 DR WormPep: F0164.2; CE03127.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DE Hypothetical protein; Oxidoreductase; NAD, Mitochondrion.
 KW NP_BIND
 FT ACT_SITE 165 165 NAD (BY SIMILARITY).
 FT ACT_SITE 11 36
 SQ SEQUENCE 258 AA; 27143 MW; 86BF2568EE6902B3 CRC64;

Query Match 57.1%; Score 748; DB 5; Length 258;
 Best Local Similarity 59.9%; Pred. No. 2.5e-44;
 Matches 154; Conservative 34; Mismatches 67; Indels 2; Gaps 1;
 OY 3 AACRSYKGLAVITGASGLGATATRLVGGASAVLLDLPNSGGEAOKKGNVCV 62
 DB 2 SALRSTKGLVAVITGASGLGATATRLVGGASAVLLDLPNSGGEAOKKGNVCV 59
 OY 63 ADVTSSEKDVOTATLAKGKRGVAVNCGIYVASKTYNLKGGTHTLEDFORVLDV 122
 DB 60 ASVTSSEKDVOTATLAKGKRGVAVNCGIYVASKTYNLKGGTHTLEDFORVLDV 119

90 285.5 21.8 254 16 09RT26 09rt26 deinosoccus
91 285 21.8 255 16 09PCQ2 09pcq2 xyliella fas
92 284.5 21.7 246 2 09E519 09e519 streptomys
93 284.5 21.7 257 16 09WYD3 09wyd3 thermotoga
94 283.5 21.7 253 16 09CH41 09ch41 lactococcus
95 283.5 21.7 256 17 08WT5 08wt5 methanosarc
96 283 21.6 252 16 092PPO 092ppo rhizobium m
97 283 21.6 275 16 09K4H0 09k4h0 streptomyc
98 282.5 21.6 272 16 099RG1 099rg1 staphylococ
99 282.5 21.6 521 16 09A7A9 09a7a9 caulobacter
100 282 21.5 306 10 091W34 091w34 arabidopsis

ALIGNMENTS

RESULT 1
096HD5 ID PRELIMINARY; PRT; 252 AA.

AC 096HD5: 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DR Similar to hydroxyacyl-coenzyme A dehydrogenase, type II.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
EMBL: BC008708; AA08708.1; -
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
KM Oxidoreductase.
SQ SEQUENCE 252 AA; 25984 MW; F36B71070CE872D CRC64;

Query Match 95.5%; Score 1250.5; DB 4; Length 252;

Best Local Similarity 96.6%; Pred. No. 4.1e-79;

Matches 252; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

0Y 1 MAACRSYKGLVAIVTGGASGLGLATAEELVGGASAVLIDLPSNGGEPAQAKKLGNNCF 60
DB 1 MAACRSYKGLVAIVTGGASGLGLATAEELVGGASAVLIDLPSNGGEPAQAKKLGNNCF 60
0Y 61 APADVTSEKDYQATALAKKFGKGRVDVAVNCAGIYVASKITNKKGGTHTEDEFORVLDV 120
DB 61 APADVTSEKDYQATALAKKFGKGRVDVAVNCAGIYVASKITNKKGGTHTEDEFORVLDV 120
0Y 121 NLMGFNVIRLVAGEMGQNEPDGQGRGVITNTASVAEFGVGGAAVSASKGGIVGWT 180
DB 121 NLMGFNVIRLVAGEMGQNEPDGQGRGVITNTASVAEFGVGGAAVSASKGGIVGWT 180
0Y 161 PIARDLAPIGIRVMTAPGIFGTPPLTSLPERKCNFLASQVPPSPRLGDPAPAYAHLYVAI 240
DB 161 PIARDLAPIGIRVMTAPGIFGTPPLTSLPERKCNFLASQVPPSPRLGDPAPAYAHLYVAI 240
0Y 181 PIARDLAPIGIRVMTAPGIFGTPPLTSLPERKCNFLASQVPPSPRLGDPAPAYAHLYVAI 231
DB 181 PIARDLAPIGIRVMTAPGIFGTPPLTSLPERKCNFLASQVPPSPRLGDPAPAYAHLYVAI 231
0Y 241 IENPFLNGEVIIRLDGAIKMP 261
DB 241 IENPFLNGEVIIRLDGAIKMP 252

RESULT 2
099N15 ID PRELIMINARY; PRT; 261 AA.
AC 099N15:
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Short chain L-3-hydroxyacyl-CoA dehydrogenase.
GN HSD17B10 OR SCHAD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21098701; PubMed=1165016;
RA He X.Y., Merz G., Chu C.H., Lin D., Yang Y.Z., Mehta P., Schulz H.,
RA Yang S.Y.;
RT Molecular cloning, modeling, and localization of rat type 10 17beta-
hydroxysteroid dehydrogenase.*
RL Mol. Cell. Endocrinol. 171:89-98(2001).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
EMBL: AF233685; AA15008.1; -
DR HSSP: O70351; 1E6W.
DR MGD: MGI:133871; Hsd17B10.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PROSITE: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KM Oxidoreductase.
SQ SEQUENCE 261 AA; 27273 MW; F371ED8A15FCEFAF CRC64;

Query Match 88.4%; Score 1157; DB 11; Length 261;

Best Local Similarity 87.7%; Pred. No. 1.3e-72;

Matches 229; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

0Y 1 MAACRSYKGLVAIVTGGASGLGLATAEELVGGASAVLIDLPSNGGEPAQAKKLGNNCF 60
DB 1 MAACRSYKGLVAIVTGGASGLGLATAEELVGGASAVLIDLPSNGGEPAQAKKLGNNCF 60
0Y 61 APADVTSEKDYQATALAKKFGKGRVDVAVNCAGIYVASKITNKKGGTHTEDEFORVLDV 120
DB 61 APADVTSEKDYQATALAKKFGKGRVDVAVNCAGIYVASKITNKKGGTHTEDEFORVLDV 120
0Y 121 NLMGFNVIRLVAGEMGQNEPDGQGRGVITNTASVAEFGVGGAAVSASKGGIVGWT 180
DB 121 NLMGFNVIRLVAGEMGQNEPDGQGRGVITNTASVAEFGVGGAAVSASKGGIVGWT 180
0Y 161 PIARDLAPIGIRVMTAPGIFGTPPLTSLPERKCNFLASQVPPSPRLGDPAPAYAHLYVAI 240
DB 161 PIARDLAPIGIRVMTAPGIFGTPPLTSLPERKCNFLASQVPPSPRLGDPAPAYAHLYVAI 240
0Y 241 IENPFLNGEVIIRLDGAIKMP 261
DB 241 IENPFLNGEVIIRLDGAIKMP 261
RESULT 3
09CTT3 ID PRELIMINARY; PRT; 261 AA.
AC 09CTT3:
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DR Hydroxyacyl-coenzyme A dehydrogenase, type II.
CN HSD17B10 OR HADH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Thu Jun 26 06:55:12 2003

us-09-931-186-8.rsp

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 14:22:37 ; Search time 31.6667 Seconds
(without alignments)
1698.262 Million cell updates/sec

Title: US-09-931-186-8
Perfect score: 1309
Sequence: 1 MAACRSVKGLVAVITGAS.....ENPFNGEVLRLDGAIRMQP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: SP archaea:.*
2: SP bacteria:.*
3: SP fungi:.*
4: SP human:.*
5: SP invertebrate:.*
6: SP mammal:.*
7: SP mhc:.*
8: SP organelle:.*
9: SP phage:.*
10: SP plant:.*
11: SP rodent:.*
12: SP virus:.*
13: SP vertebrate:.*
14: SP unclassified:.*
15: SP viirus:.*
16: SP bacteriophage:.*
17: SP archaea:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1250.5	95.5	252	4	Q96HDS
2	1157	88.4	261	11	Q99N15
3	1153	88.1	261	11	Q9CYT3
4	993	75.9	196	4	Q8RCV9
5	748	57.1	258	5	Q19102
6	720	53.0	255	16	Q810T0
7	711	54.3	255	16	Q81B50
8	689.5	52.7	252	16	Q8XWEO
9	671.5	51.3	250	16	Q06544
10	670	51.0	255	16	Q92YS1
11	667	51.0	253	16	Q98HM4
12	652	49.8	255	2	Q9AHY1
13	642	49.0	257	16	Q8UFI2
14	607	46.4	126	11	Q9DCX5
15	603.5	46.1	264	5	Q812L7
17	386	29.5	443	2	Q93S3J
18	373.5	28.5	246	16	Q8XJH1
19	355.5	27.2	244	16	Q99YD6
20	355	27.1	252	16	Q9HW15
21	343.5	26.2	249	16	Q97DA6
22	337.5	25.8	247	16	Q8R9W0
23	335.5	25.6	297	3	Q42774
24	334.5	25.6	251	16	Q8YV10
25	334.5	25.5	246	16	Q9KA03
26	332	25.4	248	16	Q9K636
27	326.5	24.9	248	2	Q9KJF1
28	325.5	24.9	243	16	Q9FBC3
29	324.5	24.8	243	16	Q9CHP7
30	324.5	24.8	260	16	Q880F8
31	323.5	24.7	260	4	Q96KR9
32	322	24.6	271	10	Q94G09
33	322	24.6	261	13	Q8U0M4
34	322	24.6	262	2	Q919F8
35	321	24.5	263	16	Q9KYM4
36	320	24.4	271	10	Q94G10
37	318.5	24.3	261	6	Q8RMM4
38	317.5	24.2	246	2	Q9EX74
39	317	24.2	258	2	Q9F8V0
40	317	24.2	299	17	Q97UK6
41	314.5	24.0	259	16	Q8U616
42	313.5	23.9	240	17	Q9UY54
43	312.5	23.9	313	2	Q93HC0
44	312	23.8	237	4	Q8WTW8
45	311.5	23.8	249	2	Q9AUT2
46	311.5	23.8	296	16	Q9ABX6
47	311	23.8	247	16	Q9PF16
48	311	23.8	262	16	Q8YD94
49	310	23.7	267	10	P93697
50	309.5	23.6	244	16	Q8ZFT5
51	309	23.6	253	16	Q8U759
52	308.5	23.6	260	17	Q8U3B3
53	306	23.4	256	16	Q8ZB06
54	303.5	23.2	236	11	Q91VT4
55	303.5	23.2	247	16	Q8U690
56	303	23.1	248	16	Q8U9B5
57	302.5	23.1	249	2	Q9LBG5
58	302	23.1	263	2	Q9S5E7
59	302	23.1	273	2	Q9F5T1
60	301.5	23.0	247	16	Q9ZAK1
61	301	23.0	247	2	Q9ZEP3
62	300.5	22.9	296	5	Q9XX28
63	300	22.9	250	2	Q56840
64	298	22.8	252	17	Q97UA4
65	296.5	22.7	538	16	Q33339
66	296.5	22.7	255	16	Q8VW75
67	296	22.6	245	16	Q8TDM1
68	295.5	22.6	254	16	Q92PP8
69	295	22.5	260	16	Q9ZPB1
70	294	22.5	255	17	Q9HQ41
71	294	22.5	265	16	Q9S2E4
72	293.5	22.4	267	2	Q9LBG2
73	291	22.2	255	16	Q8RPG3
74	291	22.2	258	16	Q930L5
75	291	22.2	315	10	Q949M3
76	291	22.2	320	10	Q93X62
77	290.5	22.2	270	4	Q9UKJ3
78	290.5	22.2	270	4	Q9UPX1
79	290	22.2	246	2	Q93HB3
80	290	22.2	272	16	Q8VHE0
81	290	22.2	328	10	Q93X67
82	289.5	22.1	405	16	Q98AS0
83	288	22.0	243	16	Q8RG25
84	287.5	22.0	303	10	Q93QF0
85	287.5	22.0	303	10	Q9SCU0
86	286.5	21.9	244	16	Q8X815
87	286.5	21.9	245	16	Q8RDP9
88	286.5	21.9	245	2	Q9R8B0
89	286.5	21.9	245	10	Q9R8B0
90	286.5	21.9	245	10	Q9R8B0
91	286.5	21.9	245	10	Q9R8B0
92	286.5	21.9	245	10	Q9R8B0
93	286.5	21.9	245	10	Q9R8B0
94	286.5	21.9	245	10	Q9R8B0
95	286.5	21.9	245	10	Q9R8B0
96	286.5	21.9	245	10	Q9R8B0
97	286.5	21.9	245	10	Q9R8B0
98	286.5	21.9	245	10	Q9R8B0
99	286.5	21.9	245	10	Q9R8B0
100	286.5	21.9	245	10	Q9R8B0

Thu Jun 26 06:55:09 2003

us-09-931-186-6.rag

Page 17

QY 129 IRLVAGEMGONBPDGGRGVTINTASVAFEGOVQAAYSASKGIYGMTLPIARDLAP 188
Db 124 IQAITEGF-----DKLGHGKTIINATSOAGVEGNAGLSIXSSTKFAVRGLTQYAADLAE 178
QY 189 IGIRVMTIAPGLFGLTSLPEKVCNFLASQVFP-----SRIGDPAEYA 234
Db 179 KNTIVNAFAPGIYETPMMKGIKAEK---LAENNQPMWGWKQFTDQIALKRLSKPEEYVA 234
QY 235 HLYQAI--ENPFLNGEVIRLDCAIR 258
Db 235 NVVSFLAGSDSDYITGOTIIVDGMR 260

Search completed: June 23, 2003, 14:28:30
Job time : 41.6667 secs

RESULT 24
ABP39667
ID ABP39667 standard; Protein; 263 AA.
XX
AC ABP39667;
XX
DT 24-JUL-2002 (first entry)
XX
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4512.
XX
KM Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
XX
KW antibacterial; gene therapy.
XX
OS Staphylococcus epidermidis.
XX
PS US6380370-B1.
XX
PD 30-APR-2002.
XX
PE 13-AUG-1998; 98US-0134001.
XX
PR 14-AUG-1997; 97US-055779P.
XX
PR 08-NOV-1997; 97US-064964P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Doucette-Stamm LA, Bush D;
XX
DR WPI: 2002-381255/41.
XX
DR N-PSDB: ABN92212.
XX
PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis
XX
PS peptide, useful for diagnosing and treating bacterial infections -
XX
PS Disclosure: SEQ ID 4512; 267pp; English.
XX
CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
XX
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
XX
CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
XX
CC antibacterial activity and can be used in gene therapy. The sequences
XX
CC can also be used in the diagnosis and treatment of bacterial infections,
XX
CC particularly S. epidermidis infections. The sequences can be used to
XX
CC screen for compounds able to interfere with the S. epidermidis life
XX
CC cycle or inhibit S. epidermidis infection.
XX
CC N.B. The sequence data for this patent did not form part of the printed
XX
CC specification, but was obtained in electronic format directly from the
XX
CC USPTO web site.
XX
SQ Sequence 263 AA;
XX

Query Match 22.6%; Score 295; DB 23; Length 263;
Best Local Similarity 32.3%; Pred. No. 8e-20;
Matches 86; Conservative 42; Mismatches 104; Indels 34; Gaps 6;

DB 12 VAVITGASGLGATTAERLVGOGASAVLLDLPNSGGEAQAOKL--GNNVFAPADVTSE 68
11 VAVITGASGLGATTAERLVGOGASAVLLDLPNSGGEAQAOKL--GNNVFAPADVTSE 68
10 VAVITGASGLGATTAERLVGOGASAVLLDLPNSGGEAQAOKL--GNNVFAPADVTSE 68
9 KDVOTATLAKKGFGRVAVNAGIAVASKTYNLKKGOTHTLEDQRLVDVNLMTFNV 128
8 KDVOTATLAKKGFGRVAVNAGIAVASKTYNLKKGOTHTLEDQRLVDVNLMTFNV 128
71 DOVFSVLNQVYEHFDLNLVNNAGLGPMTPI-----ESVTPQFNQVAVNAGVFWG 124
129 IRLVAGMEQNEPDDGGGQGVILNTASVAAFEGQGAASGAGIYGMTLPIARDIAP 188
125 IQALTEGF-----DLGHGKRIINATSGAGVGNAGLSLSTKRAVAGLQVAAADLAE 179
189 IGRVMTATPGLFGFPLLTSLPEKVCNLAQVPP-----SRLDPAEYA 234
180 KNTITNAPAGIETVPMKKGIAEK---LAEBNNQPMEMGKQOTDQIALKRLSKPEDEYA 235
235 HLVOALIT--ENPFLNGEVIKLDGAIR 258

DB 236 NVVSLAGSDSDYINGCTIIVDGMR 261

RESULT 25
AAG83032
ID AAG83032 standard; Protein; 262 AA.
XX
AC AAG83032;
XX
DT 03-SEP-2001 (first entry)
XX
DE S. epidermidis open reading frame protein sequence SEQ ID NO:3158.
XX
KM Staphylococcus epidermidis SRI strain; infection; diagnosis;
XX
KW vaccination; endocarditis.
XX
OS Staphylococcus epidermidis.
XX
PS WO200134809-A2.
XX
PD 17-MAY-2001.
XX
PE 09-NOV-2000; 2000KO-US30782.
XX
PR 09-NOV-1999; 99US-0164258.
XX
PA (GLAXO) GLAXO GROUP LTD.
XX
PI Kimmerly WJ;
XX
DR WPI: 2001-316495/33.
XX
DR N-PSDB: AAG83882.
XX
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX
PS useful for vaccinating against infections, e.g. endocarditis -
XX
PS Claim 18; Page 833; 2188pp; English.
XX
CC AAG83304 to AAG83970 represent nucleic acids (I) encoding polypeptides
XX
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis -
XX
CC (I) and (II) can have antibacterial activity and therefore can be used
XX
CC in vaccination. The nucleic acids (I) may be used to produce the
XX
CC S. epidermidis polypeptides (II) via the production of vectors
XX
CC containing them which are used to produce host cells which express the
XX
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
XX
CC used to vaccinate subjects and to raise antibodies against the bacteria.
XX
CC The polypeptides may also be used to assay for other inhibitors of their
XX
CC activity and therefore identify compounds that may be used for the
XX
CC treatment of S. epidermidis infections, e.g. endocarditis. AAG83771 to
XX
CC AAG85090 represent specifically claimed S. epidermidis genomic DNA
XX
CC polynucleotide sequences from the present invention. AAG85091 to
XX
CC AAG85098 represent oligonucleotide sequences and primers which are used
XX
CC in the exemplification of the present invention.
XX
CC N.B. The present invention specifically claims all the polynucleotide
XX
CC sequences given in the sequence listing of the present specification,
XX
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
XX
CC though sequences are given in the disclosure for SEQ ID NO:4455 to 4472,
XX
CC no sequences are present for SEQ ID NO:4455 to 4464.

Sequence 262 AA;

Query Match 22.5%; Score 294; DB 22; Length 262;
Best Local Similarity 32.3%; Pred. No. 9.9e-20;
Matches 86; Conservative 41; Mismatches 105; Indels 34; Gaps 6;

DB 12 VAVITGASGLGATTAERLVGOGASAVLLDLPNSGGEAQAOKL--GNNVFAPADVTSE 68
11 VAVITGASGLGATTAERLVGOGASAVLLDLPNSGGEAQAOKL--GNNVFAPADVTSE 68
10 VAVITGASGLGATTAERLVGOGASAVLLDLPNSGGEAQAOKL--GNNVFAPADVTSE 68
9 KDVOTATLAKKGFGRVAVNAGIAVASKTYNLKKGOTHTLEDQRLVDVNLMTFNV 128
8 KDVOTATLAKKGFGRVAVNAGIAVASKTYNLKKGOTHTLEDQRLVDVNLMTFNV 128
70 DOVFSVLNQVYEHFDLNLVNNAGLGPMTPI-----ESVTPQFNQVAVNAGVFWG 123

```
XX 25-OCT-2000 (first entry)
XX
XX Bacillus megaterium 3-keto-acyl-CoA reductase Phab.
XX
XX Polyydroxyalkanoate; polyydroxybutyrate; transgenic plant; Phab.
XX 3-keto-acyl-CoA reductase.
XX
XX Bacillus megaterium.
XX
XX WO200040730-A1.
XX
XX 13-JUL-2000.
XX
XX 07-JAN-2000; 2000WO-US00364.
XX
XX 07-JAN-1999; 99US-0115592.
XX
XX (UYMA-) UNIV MASSACHUSETTS.
XX
XX Cannon MC, Cannon FC, Mccool CJ, Valentin HE, Gruys KJ;
XX
XX WPI; 2000-532624/48.
XX
XX N-PSDB; AAA50142.
XX
XX New nucleic acid fragment encoding proteins involved in
XX polyydroxyalkanoate (PHA) biosynthesis, useful in the production of
XX transgenic plants or recombinant plant cells which can express PHAs
XX such as polyydroxybutyrate.
XX
XX Claim 85; Page 137-138; 153pp; English.
XX
XX The present sequence is that of Phab, a 3-keto-acyl-CoA-reductase
XX protein of Bacillus megaterium. The sequence was deduced from an
XX open reading frame identified in an isolated 7,916 bp fragment of
XX B. megaterium strain 11561 genomic DNA (see AAA50142). The 7,916 bp
XX DNA fragment includes genes encoding proteins (see AA195743-47)
XX involved in polyydroxyalkanoate (PHA) biosynthesis. Nucleic acids
XX encoding these proteins are useful for creating transgenic plants or
XX recombinant host cells which have the capability of expressing PHAs
XX such as polyydroxybutyrate, polyydroxyvalerate,
XX polyydroxyhexanoate, polyydroxyoctanoate, polyydroxydecanoate or
XX their copolymers. Claimed methods for preparing a PHA involve
XX obtaining a plant or a cell comprising a nucleic acid encoding
XX a 3-keto-acyl-CoA reductase (especially the present sequence), and
XX a nucleic acid encoding a PHA synthase (see AA195747), and growing
XX the plant or cell under conditions suitable for PHA production.
XX
XX Sequence 247 AA;
SQ
Query Match 23.1%; Score 301; DB 21; Length 247;
Best Local Similarity 23.1%; Pred. No. 2e-20; Mismatches 9;
Matches 78; Conservative 59; Mismatches 93; Indels 38; Gaps 9;
7 SVKGVAVITGASGLGATERTLVGGG-----ASAVLDLPNSGGEAQAOK 53
3 TLQGVAVITGSGSKGIGAITRELASNGVAVVNNSSKSAEAIKIKNGGEA--- 58
54 LGNNVVEFADVTSEKDVOTALAKKFGFVDAVAVNAGIAVASKITNLRK-GQTHLE 112
59 ----IAVQADVSYDQAKHLEETKAFGQDIDIVNAGI--TRDSFKLEB---E 106
113 DEQFVLVDNLMTGFENVILVAGEMQNEPDGQGGVINTASVAAFEQYGOAAYSASK 172
107 DMKAKVIDNLSHYNTTSALHLHLESE---QGR---VINISSIIGQGGGQFNYSASK 160
173 GGIVKMTPLIARDLAPIGIRVWTTPAGLFGTPLLTSLPEKCNFLASVPPPSRLGDAE 232
161 AGMLGFTSLALELAKTGVTVNALCPGFETEMWAIPEDEVRAKIVAKIP-TRRLGHAEE 219
233 YAH-LVOAIIENPFLNGEVIIRLDGAI 259
220 IARGVYIAKDGAYITTGQOLINISGLVM 247
DB
```

```
RESULT 23
AAB47459
ID AAB47459 standard; Protein; 267 AA.
XX
XX AAB47459;
AC
XX 13-DEC-2001 (first entry)
DT
XX Levodione reductase.
DE
XX Levodione reductase; homologous subunit; levodione; primer; amplify;
XX (4R,6R)-4-hydroxy-2,2,6-trimethylcyclohexanone; actinol; zeaxanthin;
XX PCR; polymerase chain reaction.
XX
XX Corynebacterium aquaticum.
OS
XX EP1122315-A1.
XX
XX 08-AUG-2001.
PD
XX 29-JAN-2001; 2001EP-0101940.
PF
XX 01-FEB-2000; 2000EP-0101665.
PR
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Shimizu S, Wada M;
XX
XX WPI; 2001-551347/62.
XX
XX N-PSDB; AAA43285.
DR
XX
XX New Corynebacterium aquaticum levodione reductase gene, useful for
XX producing levodione reductase for converting levodione to actinol,
XX which is a useful chiral building block of naturally occurring
XX optically active compounds.
XX
XX Claim 3; Page 15-16; 19pp; English.
XX
XX This sequence shows levodione reductase. Levodione reductase has a
XX relative molecular mass of 142-155kD +/- 10kD consisting of four
XX CC homologous subunits each having a molecular mass of 36kD +/- 5kD. This
XX CC enzyme converts levodione to (4R,6R)-4-hydroxy-2,2,6-trimethyl-
XX cyclohexanone (actinol), which is a useful chiral building block of
XX naturally occurring optically active compounds such as zeaxanthin.
XX
XX Sequence 267 AA;
SQ
Query Match 22.8%; Score 297.5; DB 22; Length 267;
Best Local Similarity 31.8%; Pred. No. 4.7e-20;
Matches 84; Conservative 46; Mismatches 97; Indels 37; Gaps 9;
12 VAVITGASGLGATERTLVGGASAVLDLPNSGGEAQAOKL-----GNVYFAADVT 66
15 VVITGGSGGLGATERTLVRLAEAGAKSLVDVSSGELEASRAVLETPADVAELTVADVS 74
67 SEKDVOFALAKKFGFVDAVAVNAGIAVASKITNLRKQTHLEDFQFVLVDNLMTGF 126
75 DEAOVEAYVATTEFRERIDGFFNNAGIECKQ-----NPRESSTADEFDVSINLRGV 129
127 ----NVIRLVAGEMQNEPDGQGGVINTASVAAFEQYGOAAYSASKGIVGNTLPI 182
130 LGLEKVLKIMR-----EQQS--GWWVTASVGGIRGIGNOSGYAAAKHGVAULTRNS 179
183 ARDLAPIGIRVMTAPLFGTPLLTSL-----PEKVC-NFLASQVPPPSRLGDAEY 233
180 AVEGGRGIINMATAIPATIPVENSMMKLDPENRKAABEET--QVNSKRYGEAPEI 237
234 AHLVQAIIEEN--PFLNGEVIIRLDG 255
238 AAVVAFLSDDASVYNAVTVPIDG 261
DB
```

```

XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX
PS Example 3; Seq ID No 10921; 511pp; English.
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 245 AA;
XX
XX Query Match 23.7%; Score 308.5; DB 22; Length 245;
XX Best Local Similarity 33.3%; Pred. No. 3.8e-21;
XX Matches 83; Conservative 38; Mismatches 109; Indels 19; Gaps 5;
XX
QY 15 TTGASGAGLTAERLVGOGASAVILD----LPNSGGEAQAAGKGNVYFAPADVTSEKD 70
DB 10 TGTGTGICAKAVAAFAKAGANIVNGRSEITPEGRQLEEA--FEVKCIGSGDISDPDA 67
QY 71 VGTALALAKGKRGADVAVNCAGIYVASTYVNLKGGQTHLEDFQVLDVNLMTGFNVIR 130
DB 68 AGEMIAQATVDQJGSDIILVNNMGIT-----NDKLLRLTKEDFNACLDINLVGFNNMQ 121
QY 131 LVAGEGQNEPDGQGRGVYINTASYAAEGVQGAASASAGSAGIVGHTLPRIADLP 190
DB 122 QAVKRMKKO-----RSGRIINMASVSGLMGVGQANVAAASAGVGGFESKVAKEVAPRG 175
QY 191 IRMTAPGFGFGLTSLPEKVCNPLASQVFPFSLGDPAPYAHVQAIIENPFLNGEV 250
DB 176 ITGNALAPGFIQEMTDVLSERKTKQMNQIPLQT-FQGVEDVAAATRAIRLAKSPYITGCV 234
QY 251 IRLDGAIRM 259
DB 235 VNVGGGLVM 243
XX
XX RESULT 21
XX ABB48892 standard; Protein; 247 AA.
XX
XX ABB48892;
XX
XX 05-FEB-2002 (first entry)
XX
XX DE Listeria monocytogenes protein #1596.
XX
XX KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
XX vitamin B12; bacterial infection; disease.
XX
XX OS Listeria monocytogenes.
XX
XX WO200177335-A2.
XX
XX 18-OCT-2001.
XX
XX * 11-APR-2001; 2001WO-FR01118.

```

```

XX
XX 11-APR-2000; 2000FR-0004629.
XX
XX (INSP ) INST PASTEUR.
XX
XX Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
XX Dussurget O, Cheouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
XX Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JH;
XX Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
XX Chakraborty T, Doman E, Hain T, Berche P, Charbit A, Durant L;
XX Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
XX Madueno E, De Pablo B, Wehland J, Kaerst U, Entian K, Hauf J;
XX Rose M, Voss H;
XX
XX MPI; 2002-010914/01.
XX
XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
XX and prevention of Listeria and related bacterial infections, and
XX related polypeptides -
XX
XX PS Claim 6; SEQ ID No 1597; 192pp; French.
XX
XX The present invention relates to the genome sequence of Listeria
XX monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
XX it are useful for selecting probes and primers for detecting genes in L.
XX monocytogenes and related organisms, and for studying genetic
XX polymorphisms and other genomes. The present sequence is a protein
XX encoded by the genome sequence of the present invention. Proteins
XX expressed from the genome sequence are useful for raising specific
XX antibodies, identification of L. monocytogenes and related organisms, and
XX for biosynthesis and biodegradation, especially biosynthesis of Vitamin
XX B12. The genome sequence and proteins encoded by it are also useful for
XX selecting compounds that regulate gene expression and cell replication
XX and modulate L. monocytogenes-related diseases. In addition, the genome
XX sequence and proteins encoded by it are useful in pharmaceutical and
XX vaccines compositions for the treatment or prevention of infections by L.
XX monocytogenes and related organisms.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 247 AA;
XX
XX Query Match 23.7%; Score 308.5; DB 23; Length 247;
XX Best Local Similarity 32.3%; Pred. No. 3.8e-21;
XX Matches 86; Conservative 45; Mismatches 102; Indels 33; Gaps 7;
XX
QY 7 SVKGIYAVITGASGLIATAEERLVGOGASAVILDLPSNGGEAQA---KKL---GNNV 58
DB 2 TLGGVAVAVITGSGNSIGRIDINILAKGANIFF---NNGSPFAAEETAKVAHEHGEV 57
QY 59 VFAPADVTSEKDVQATALALAKGKRGADVAVNCAGIYVASTYVNLKGGQTHLEDFQVRL 118
DB 58 EAMKANVAIADVDVAFEFKQAEIRGRVDIILVNNGIFRDNLMRKE-----DEWDV 111
QY 119 DVNLMTGFNVIRLVAGEGQNEPDGQGRGVYINTASYAAEGVQGAASASAGSAGIVGM 178
DB 112 NINLKGITLCTKAVSRIMKKO-----RAGKIINMASVYGLIGNAGQANVYASRAGYIGL 165
QY 179 TLPIARDLAPIGIRVMTAPGLFGTLPILTSLEKVCNPLASQVFPFSLGDPAPYAHVQ 238
DB 166 TKTAREILAPRGINAVNAVAPGFIITDMDKIDKTEKRLMAQIP---LGA YGTTEIDIAN 221
QY 239 AII-----ENPFLNGEVIRLDGAIRM 259
DB 222 AVLFLASDAKSIITIGQTLSDVGGMYM 247
XX
XX RESULT 22
XX AAY95746
XX
XX AAY95746 standard; Protein; 247 AA.
XX
XX AAY95746;

```


07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Dirmancic RT, Zhang J, Chen R, Xue AJ, Wang J;
 XX
 XX WPI: 2001-589934/66.
 DR N-PSDB: AAS45056.
 XX
 XX Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 XX
 XX Example 4; SEQ ID NO 325; 107bp; English.
 PS
 XX The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC and lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC anesthetic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention.
 CC
 XX Sequence 237 AA:

Query Match 23.9%; Score 312; DB 22; Length 237;
 Best Local Similarity 31.6%; Pred. No. 1.7e-21;
 Matches 80; Conservative 42; Mismatches 105; Indels 26; Gaps 5;

QY 12 VAVITGGASGLARERLVGGASAVLIDLPNSGSGAQLGNVYFAPADYSEKD 71
 DB 4 VCAVGGSGRGIRAAVAQIMARKGYRLAVARNLEGAAGAGDLGSDHAFSCDAKEDV 63
 QY 72 QFALALAKGKFRVAVVNCAGI-----AVASKYITLKKGQTHLEDFQRYLVDMNGTF 126
 DB 64 QMTFEMEMHRLRVNFTVMAAINDGLVTRKT-----EDWVSQJHTNLISM 112
 QY 127 NVIRLVAGKGNRDPGGQGVYINTASVAFPEQVGGAASAKSGKGVGNTLTDL 186
 DB 113 LTCKAAMRTMD-----QGSGIYVWGSIVGLKNGSGOSVYSASKGGLVGSFALANEV 166

QY 187 APGIRVMTIAPGLFPTLTSLPKVCNFTLACVPPSRRLGDAEVAHLVQATIENTPFL 246
 DB 167 AKRKIRRVNVAAPGFPHITMDTKDE---HLKKNFTL-GRGETLEVAAHVAVPLESEPTI 222
 QY 247 NGEVTRLDGAIKM 259
 DB 223 TGHVAVVDGIGLOT 235

RESULT 18
 AAB19928
 ID AAB19928 standard; Protein; 237 AA.
 XX
 XX AAB19928;
 XX
 XX 19-MAR-2001 (first entry)
 DT
 XX Human oxidoreductase OXRD-3.
 DE
 XX OXRD-3; human; oxidoreductase; dehydrogenase; cell proliferation;
 KM neurological disease; smooth muscle disease; autoimmune disease;
 KM inflammation; antiproliferative; neuroprotective;
 KM immunosuppressive; antiinflammatory; therapy; diagnosis.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH
 FT Misc-difference 66
 FT Misc-difference 95
 FT Misc-difference 114
 FT Misc-difference 114
 FT /note- "O-phosphorylated"
 FT /note- "O-phosphorylated"
 FT /note- "O-phosphorylated"
 FT /note- "short-chain dehydrogenase signature"
 PN MO200071679-A2.
 XX
 XX 30-NOV-2000.
 PD
 XX 19-MAY-2000; 2000MO-US13879.
 PF
 XX 20-MAY-1999; 99US-0135049.
 PR 27-MAY-1999; 99US-0136740.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 XX
 PI Yue H, Tang YT, Baughn MR, Lu DM;
 XX
 DR WPI: 2001-025146/03.
 DR N-PSDB: AAA89187.
 XX
 PT New human oxidoreductase proteins useful for diagnosing, treating or
 PT preventing proliferative, neurological, genetic, smooth muscle,
 PT autoimmune or inflammatory disorders associated with abnormal
 PT expression of oxidoreductase proteins -
 PT
 XX
 XX Claim 1(a): Page 83; 95pp; English.

The present sequence is that of human oxidoreductase OXRD-3, as deduced from a cDNA clone (see AAA89187) isolated from a lung tumour cDNA library. The protein shows homology to Escherichia coli 3-oxoacyl-(acyl)-carrier protein, and includes a short-chain dehydrogenase signature. OXRD-3 is expressed in nervous, reproductive, cardiovascular and gastrointestinal tissue, and may be involved in cell proliferation and inflammation. The invention provides OXRD-1 to -8 polypeptides (see AAB19926-33) and polynucleotides (see AAA89185-92). It also provides methods for using these polypeptides and polynucleotides for diagnosing, treating or preventing disorders associated with expression of OXRD, especially cell proliferative, neurological, genetic, smooth muscle, and autoimmune/inflammatory disorders. The proteins can also be used to screen for agonists and antagonists useful for treating these conditions, while

PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 PA (HXSE-) HXSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P,
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 XX WPI: 2001-589934/66.
 DR N-PSDB; AAS45244.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 XX
 PS Example 2; SEQ ID No 701; 107pp; English.
 XX
 CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention.
 XX
 SO Sequence 257 AA:
 Query Match 24.3%; Score 317; DB 22; Length 257;
 Best Local Similarity 31.5%; Pred. No. 6.3e-22;
 Matches 82; Conservative 42; Mismatches 110; Indels 26; Gaps 5;

DB 180 RALAEVARKKIRVNVVAPGVHTMDTRDKEE--HUKNIPL-GREGTEVAHAAYF 235
 QY 240 ILENPLNGEYTRLDGAIRM 259
 DB 236 LIESPITGSHVLYVDGIDL 255
 RESULT 15
 AAMS0255
 ID AAMS0255 standard; Protein; 237 AA.
 XX
 XX AAMS0255;
 AC
 XX 21-JAN-2002 (first entry)
 DT
 XX Human dehydrogenase 21509.
 DE
 XX
 KW Dehydrogenase; human; ovarian cancer; colon cancer; lung cancer;
 KW liver cancer; metastasis; antitumour; therapy; diagnosis.
 OS Homo sapiens.
 XX
 XX Key
 FH Location/Qualifiers
 FT Domain
 FT 3..229
 FT /note="short-chain alcohol dehydrogenase domain"
 FT 148..158
 FT /note="short-chain alcohol dehydrogenase family
 FT signature"
 FT 114..116
 FT /note="O-phosphorylated by protein kinase C"
 FT 66..69
 FT /note="O-phosphorylated by casein kinase II"
 FT 95..98
 FT /note="O-phosphorylated by casein kinase II"
 FT 9..14
 FT /note="N-myristoylated"
 FT 38..43
 FT /note="N-myristoylated"
 FT 110..115
 FT /note="N-myristoylated"
 FT 128..133
 FT /note="N-myristoylated"
 FT 134..139
 FT /note="N-myristoylated"
 FT 153..158
 FT /note="N-myristoylated"
 FT
 XX
 XX MO200175119-A2.
 PV
 XX 11-OCT-2001.
 PD
 XX
 XX 02-APR-2001; 2001WO-US10720.
 PF
 XX 31-MAR-2000; 2000US-193920P.
 PR
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX Meyers RA, Rudolph-Owen LA;
 PI
 XX WPI: 2001-626438/72.
 DR N-PSDB; AAI70573.
 DR
 XX
 XX Novel isolated 21509 and 33770 polypeptides belonging to human
 PT dehydrogenase family members, useful for treating cancer, diabetes,
 PT atherosclerosis, glomerulonephritis, Crohn's disease, cirrhosis,
 PT multiple sclerosis -
 XX
 PS Claim 1(a); Fig 2; 146pp; English.
 PS
 XX The present sequence is that of a novel human dehydrogenase,
 CC designated 21509. The protein has a significant number of
 CC structural characteristics in common with members of the
 CC dehydrogenase/oxidoreductase family. Its expression pattern

CC acids are useful for detecting the presence of proteins essential for the
 CC viability of a bacterial cell wall in samples such as cells, tissues,
 CC biological fluids, blood, serum, nose, ear or throat swabs with ligands,
 CC and for detecting corresponding target nucleic acid molecules with
 CC complementary sequences. The nucleic acids are also useful for
 CC determining whether a genomic nucleotide sequence of interest is
 CC essential for viability of a bacterial cell or whether it resides within
 CC an operon, by integrating an exogenous nucleotide sequence comprising a
 CC portion of an open reading frame of the genomic sequence of interest
 CC (comprising 200-500 base pairs) into the genomic sequence of interest
 CC which confers a selectable phenotype to the cell, and determining cell
 CC viability with a selection agent such as chloramphenicol. The nucleic
 CC acids and proteins are also useful as vaccines and for treating bacterial
 CC infections with gene therapy and antisense therapy. The nucleic acids
 CC also enable identification of targets suitable for the treatment of
 CC antibiotic resistant bacterial infections.

XX Sequence 243 AA:

Query Match 25.3%; Score 330.5; DB 22; Length 243;
 Best Local Similarity 35.1%; Pred. No. 3.1e-23;
 Matches 88; Conservative 37; Mismatches 103; Indels 23; Gaps 6;

15 TGGAGAGLATAERLVGQASAVLLDLPNSGGE-----AQAKKLGNNVYFAPADVISE 68
 10 TGGSSGICGLATAHKAQAGANIVL-----NSRGAISELLAEFNVGKIVPISGDVSDF 65
 69 KDVQALALAKGKFGHVDVAVNCAGIAVASKTYNLRKQGTHTLEDFORYLDVNLGTRNV 128
 66 AAKRMIDDAIELGSDVAVLNNAGI--TQDTLMKM---TEAFEEKLVKYNLGAENM 119
 129 IRLVYAEEMGNEPDGQGVIIINTASVAFEGOVQOAYASAKSGIVMTPIARDLAP 188
 120 TQGVV-----KPMKARREGAIIIMSSVYGLMGNICQANYASAKGLIGFTSVAREVAS 173
 189 IGRVMTIAPGLFETPLTSLPEKVCNFIASQVPEPSRLGDPAEVAHLVQAIENPFLNG 246
 174 RTRVNVVIAAPGIESDMTALISDKIKETIAQIPM-KEFGQAEQVADLVFLAGODYLNG 232
 249 EVIRLDGAIRM 259
 233 QVVAIDGGLSM 243

RESULT 13

ABBS4087 ID ABB54087 standard; Protein; 243 AA.

XX AC ABB54087;

XX DT 16-MAY-2002 (first entry)

XX DE Lactococcus lactis protein dabG1.

XX KW Biosynthesis: biodegradation; lactic bacterium; yogurt; cheese.

XX OS Lactococcus lactis IL1403.

XX PN FR2807446-A1.

XX PD 12-OCT-2001.

XX PF 11-APR-2000; 2000FR-0004630.

XX PR 11-APR-2000; 2000FR-0004630.

XX PA (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX PI Boletine A, Sorokline A, Renault P, Ehrlich SD;

XX DR WPI; 2002-043418/06.

XX PT New nucleotide sequence useful in the identification or Lactococcus

PT lactis and related species -
 XX Claim 6; SEQ ID No 789; 2504pp; French.

XX The present invention is related to a Lactococcus lactis nucleotide
 CC sequence (AA090521) and related proteins (AB553300-AB555621). The
 CC nucleic acid sequence is useful in the detection and/or amplification of
 CC related species. The proteins of the invention are useful for the
 CC biosynthesis or biodegradation of a composition of interest. The
 CC invention helps research in lactic bacteria, particularly useful in the
 CC production of yogurt and cheese.
 CC Note: The sequence data for this patent is based on equivalent patent
 CC WO2001/77334 (published 18-OCT-2001) which is available in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 243 AA:

Query Match 24.9%; Score 324.5; DB 23; Length 243;
 Best Local Similarity 31.7%; Pred. No. 1.1e-22;
 Matches 82; Conservative 48; Mismatches 104; Indels 25; Gaps 6;

8 VKGLVAVITGGASGLATAERLVGQASAVLLDLPNSGGEAOKK-----GNVVF 60
 3 IKNNVFEVGTGTRIGKAIALQFAKASNLII-----NGSAISELLAEFTAYGAVAG 57
 61 APADVTSKDVQATALALAKGKFGHVDVAVNCAGIAVASKTYNLRKQGTHTLEDFORYLDV 120
 58 ISGDISKEDKQAVAEIETLGSDVILNNAGI--TRDGLSKMSE-----EDPEVYIKI 111
 121 NLMGTENVIRLVAGBMGNEPDGQGVIIINTASVAFEGOVQOAYASAKSGIVMTL 180
 112 NLTGAFNMTQAVL-----KPMTRARSGAIIIMSSVYGLMGNICQANYASAKGLIGFTSV 165
 181 PIARDIAPIGRVMTIAPGLFETPLTSLPEKVCNFIASQVPEPSRLGDPAEVAHLVQAI 240
 166 SIARVAVARNRVNNAAPGIESDMTEVLSKIVADAMKGQIPM-KRGMPEIATATQFL 224
 241 IENPFLNGEVRILDGAIRM 259
 225 AOEYMTGQVLTIDGVSIM 243

RESULT 14

AAU28344 ID AAU28344 standard; Protein; 257 AA.

XX AC AAU28344;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secretory protein, Seq ID No 701.

XX KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen.

XX OS Homo sapiens.

XX PN WO200166689-A2.

XX PD 13-SEP-2001.

XX PF 05-MAR-2001; 2001WO-US04942.

XX PR 07-MAR-2000; 2000US-0519705.
 19-MAY-2000; 2000US-0574454.

OS	Streptococcus pneumoniae.
XX	
PX	MO200044885-A1.
PN	
PD	03-AUG-2000.
XX	
PF	19-JAN-2000; 2000WO-US01131.
PR	27-JAN-1999; 99US-0239052.
PA	(SMR) SMITHKLINE BEECHAM CORP.
PI	Holmes DJ, Mooney J, Zhong YY, Debouck C, Jaworski DD, Wang M;
PI	Marren RL, Kosmetka AL, McDevitt D, Ingraham KA, Chalker AF;
DR	So CY, Wallis NG, Pearson SC;
XX	WPI: 2000-482971/42.
PS	N-PSTDB; AAA74684.
PT	FabG polypeptide, isolated from Streptococcus pneumoniae, is used to
PT	treat microbial diseases, identify agonists and antagonists for
PT	treating microbial infections and to detect diseases associated with
XX	microbial infections -
PS	Claim 1; Page 3; 40pp; English.
CC	The present sequence is a FabG (2-oxoacyl-acyl carrier protein
CC	reductase) polypeptide. A full length fabg gene was isolated from a
CC	Streptococcus pneumoniae 0100993 DNA library in E. coli. FabG
CC	polynucleotides and polypeptides are used for detection and treatment of
CC	microbial diseases. They may also be used to identify antagonists and
CC	agonists which can then be used to treat microbial diseases. Compounds
CC	that interfere with the initial physical interaction between a pathogen
CC	and a host have been identified. The compounds are able to prevent the
CC	adhesion of bacteria to mammalian extracellular proteins in wounds,
CC	prevent adhesion between mammalian extracellular proteins and bacterial
CC	fate proteins which mediate tissue damage and/or to block normal
CC	progression of pathogenesis in infections mediated by implantation of
CC	in-dwelling devices or other surgical techniques. The fabg
CC	polypeptides, polynucleotides, antagonists and agonists are especially
CC	useful in the treatment of Helicobacter pylori infection. They may be
CC	used to decrease H. pylori-induced cancers and to prevent, inhibit
CC	and/or cure gastric ulcers and gastritis.
XX	
SQ	Sequence 243 AA:
Query Match	25.4%; Score 331.5; DB 21; Length 243;
Best Local Similarity	35.5%; Pred. No. 2.5e+23;
Matches	89; Conservative 36; Mismatches 103; Indels 23; Gaps 6
Dy	15 ITGGAGCGLATAAERLYVGGAASAVLDDPSNGGE-----AAAKLGNNVFAADPYTSE 68
Db	10 ITSSSGIGLATAHRAAQAQANITVL-----NSRGALISELLAEFENYGIKVPPLISGVDSDF 65
QY	69 KDVOQTALALAKGFGRHVVAVNCACIIVASTYNLKKGQHTLEDFOVDLVNLMGTFNY 128
Db	66 ADAKRMIIDAIELGSDVYLANNAGI--TOOTLMKKM---TEADFERYVKVMLTAFFNW 119
QY	129 IRLVAEMGONPEPDQGCGVGINFNINFAAFEGGOGAAYASAGSGIVGTLPRIARDLAP 188
Db	120 TGSVL-----KPMKARREGALINNSSVYGLMGNINGCANYASAAGLIGTKVARAEVAS 173
QY	189 IGIRVNTAPGLFGIPLLLTSPKEVCNFLASOVPPSPSLGDPAEYLAHVLAITENPLNG 248
Db	174 RNRVRNVAPIGMIESDMETILSDKIREXTLAQIPW-KEFGOAEQVADLTVEFLGODYLTG 232
QY	249 EVTRLDAIRM 259
Db	233 QVTALDGGLSM 243

[illegible]

XX New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -

XX Claim 1; Page 3542; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B
CC Streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (1), nucleic acids encoding (1), ABN66044-ABN71516 and
CC antibodies that bind (1) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (1) are used to detect Streptococcus in a
CC biological sample. (1) is used to determine whether a compound binds to
CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (1) may be used to recombinantly produce (1) and may be
CC used in gene therapy. Antibodies to (1) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.

XX Sequence 243 AA;

XX Query Match 27 3%; Score 356; DB 23; Length 243;

XX Best Local Similarity 35.8%; Pred. No. 1.2e-23;

XX Matches 93; Conservative 42; Mismatches 99; Indels 26; Gaps 6;

XX 8 VGLVAVITGGASGIGLTAERLVGOGASAVLLDLPNSGGEAQAQKL-----GNNVVF 60

XX 3 IKGNL-FITGSTRGIGLMAHQFASLEANIYL-----NGRSALISEELVASFDTGVTVVT 56

XX 61 APADVTSEKDVOTATLALKGFGRVDVAVNCAGTAVASKTINLKGQHTLEDQRVLVD 120

XX 57 ISGDVSEASEARKNVNEAIESLGSIDVAVNNAGIT-----NDKIMLKTEDDERVAKI 110

XX 111 NLTGAFNMTQSVL-----KPKIKAROGAILINVSVGLTGNIGAGNVAASKAGIGPTK 164

XX 121 NLMGFNVRIYVAGEMGONPEPOGSGRGIINTASVAFAEGOVGAASASKSGIVGWTL 180

XX 181 PIARDIPIGIRVMTIAPGLFETPLTSLPEKVCNFTLASQVPPFSRLDPAEYAHVQAI 240

XX 165 SVAREVAARNICVNAIAFGIESDMTGVLPKMOBQIISQIPM-KRIGKAGEVAHLASF 223

XX 241 IENPFLNGEVRILDGAIKRMQ 260

XX 224 VEQDIITGCVIAIDGGMKMQ 243

XX Db

XX RESULT 8

XX AAB80670

XX ID AAB80670 standard; Protein; 243 AA.

XX AAB80670;

XX 24-DEC-1998 (first entry)

XX S. pneumoniae fatty acid biosynthesis protein.

XX Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip;

XX virulence; antibody; infection; detection; treatment; hypothetical;

XX cell wall biosynthetic; external target; minimal gene set protein.

XX 13-DEC-1996; 9605-0036281.

XX (ELIL) LILLY & CO ELI.

XX Ballz RE, Burgett SC, Dehoff BS, Hoskins JA, Jaskunas SR;

XX Mills BU, Norris FH, Peery RA, Rockey PK, Rostock PR;

XX Skatrud PL, Smith WC, Solenberg PJ, Treadway PJ;

XX Young Bellido ML;

XX WPI; 1998-348529/30.

XX Streptococcus pneumoniae nucleic acid sequences - used in DNA chips

XX for evaluating gene expression, and identification of virulence

XX genes

XX Claim 3; Page 270; 333pp; English.

XX This sequence represents a S. pneumoniae fatty acid biosynthesis

XX protein. The invention provides DNA sequences (AAB65201 to AAB65304)

XX from the Streptococcus pneumoniae genome and corresponding protein

XX sequences (AAB60605 to AAB60728). The protein sequences are classified as

XX hypothetical, cell wall biosynthetic, external target, or minimal gene

XX set proteins. A recombinant host containing a vector comprising any of

XX the above nucleic acids can be used for the recombinant expression of the

XX proteins. The invention also provides a DNA chip having arrayed on it at

XX least 15 base pair fragment of any one or more of these DNA sequences.

XX The DNA chip can be used methods for evaluating gene expression in S.

XX pneumoniae and for identifying virulence genes in S. pneumoniae.

XX Antibodies that selectively bind to the above proteins or peptide

XX fragments can be used to treat S. pneumoniae infection. The antibodies

XX can also be used to detect S. pneumoniae cells.

XX Sequence 243 AA;

XX Query Match 25 4%; Score 331.5; DB 19; Length 243;

XX Best Local Similarity 35.5%; Pred. No. 2.5e-23;

XX Matches 89; Conservative 36; Mismatches 103; Indels 23; Gaps 6;

XX 15 ITGASGIGLTAERLVGOGASAVLLDLPNSGE-----AQAKKIGNNVFAPADVISE 68

XX 10 ITGSSRGIGLAIHAKFQAQANIVL-----NSRGAISEELAEBSNGIVPISGVSDPF 65

XX 69 KDVOATLALKGFGRVDVAVNCAGTAVASKTINLKGQHTLEDQRVLVD 128

XX 66 ADARFMIDQAIAGLGSVDVAVNNAGI--TODTLMK--TADDEKYLKMLTAFVNA 119

XX 129 IRLVAGEMGONPEPOGSGRGIINTASVAFAEGOVGAASASKSGIVGWTLP 188

XX 120 TQSVL-----KPKMKAREGAILINSSVGLTGNIGAGNVAASKAGIGPTK 173

XX Db

XX RESULT 9

XX AAB15706

XX ID AAB15706 standard; Protein; 243 AA.

XX AAB15706;

XX 07-DEC-2000 (first entry)

XX Streptococcus pneumoniae FabG polypeptide.

XX Streptococcus pneumoniae; FabG; 3-oxoacyl-acyl carrier protein reductase;

XX antibacterial; cytostatic; antitumor; cancer; gastric ulcer; gastritis;

XX Helicobacter pylori infection; microbial infection.

Query Match 51.0%; Score 664.5; DB 18; Length 388;
 Best Local Similarity 55.5%; Pred. No. 1.1e-54;
 Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VGLVAIVTGGASGLTAEELVGGASAVLLDLPNSGSEBAOKKLGNNVFAADYTS 67
 DB 143 IEGRFVVTGGAASGGAASAKRLAOGKAVYLADI-----AEKDAPEGVAHACDVTD 196
 QY 68 EKDVTALALAKGKRGVAVNCAIGIAVASKTYNLKKGTHTLEDFOVLDVNLGTFN 127
 DB 197 ATAQTALATLDTRGRDLGIVNCAGIAPAEEM--LGRDGHGIDSEFAVATINLIGSFN 254
 QY 128 VRLVAGSEMGONEPPOGGORGVIINTASVAPEGOVGAAYASAKGIVGWTLEIARDLA 187
 DB 255 MARLAEAMARNEYR--GERGVYVNTASTIAADGIGVAVTAASKAGVAGWTLEIPARDLA 313
 QY 188 PIGIRVMTIAPGLFETPLLTSLPEKVCNFIASQVFPSPRLDPAEYAHVQAIIENPFLN 247
 DB 314 RGIKRVMTIAPGIEFTPMLEGLPDQVDSLGAAYVFPRLCEPSEYALHLHIITANPMLN 373
 QY 248 GEVIRLDGAIRMOP 261
 DB 374 GEVIRLDGALRMAP 387

RESULT 6
 ABP28011
 ID ABP28011 standard; Protein; 244 AA.

XX ABP28011;
 DT 02-JUL-2002 (first entry)
 XX Streptococcus polypeptide SEQ ID NO 5198.
 DE Streptococcus polypeptide SEQ ID NO 5198.
 XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;
 XX antiinflammatory; infection; vaccine; meningitis; gene therapy.
 OS Streptococcus agalactiae.
 XX MO200234771-A2.
 PN 02-MAY-2002;
 PD 29-OCT-2001; 2001WO-GB04789.
 XX 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettelin H;
 DR WPI: 2002-352536/38.
 DR N-PSDB: ABN68642.
 XX New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PI for detecting a compound that binds to the protein -
 XX Claim 1; Page 3663; 4525pp; English.
 PS The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.

SQ Sequence 244 AA;
 Query Match 28.1%; Score 366.5; DB 23; Length 244;
 Best Local Similarity 36.9%; Pred. No. 1.2e-26;
 Matches 93; Conservative 38; Mismatches 98; Indels 23; Gaps 5;

QY 15 ITGASGLGATAEELVGGASAVLLDLPNSGSE-----AQAKKLGNNVFAADYTS 68
 DB 10 ITGSSRGIGLAIHQFQOLANIVL-----NGRBEISDILAEADIGVAVIALSGVSSF 65
 QY 69 KDVTALALAKGKRGVAVNCAIGIAVASKTYNLKKGTHTLEDFOVLDVNLGTFN 128
 DB 66 EDANRMKIKELIASLSGVYLVNNAGIT-----NDKIMLMTVEDESVYKINLTGAFNM 119
 QY 129 IRLVAGSEMGONEPPOGGORGVIINTASVAPEGOVGAAYASAKGIVGWTLEIARDLA 188
 DB 120 TQSVL-----KPKTRKRGAIINISSVGLTGVGOANAAASKAGLIGTKSVAREVAA 173
 QY 189 IGIKRVMTIAPGLFETPLLTSLPEKVCNFIASQVFPSPRLDPAEYAHVQAIIENPFLN 248
 DB 174 RGIKRVMTIAPGIEFTPMLEGLPDQVDSLGAAYVFPRLCEPSEYALHLHIITANPMLN 373
 QY 249 EVIRLDGAIRMOP 260
 DB 233 QVIRLDGQMTWQ 244

RESULT 7
 ABP27345
 ID ABP27345 standard; Protein; 243 AA.

XX ABP27345;
 DT 02-JUL-2002 (first entry)
 XX Streptococcus polypeptide SEQ ID NO 3866.
 DE Streptococcus polypeptide SEQ ID NO 3866.
 XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;
 XX antiinflammatory; infection; vaccine; meningitis; gene therapy.
 OS Streptococcus pyogenes.
 XX MO200234771-A2.
 PN 02-MAY-2002;
 PD 29-OCT-2001; 2001WO-GB04789.
 XX 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettelin H;
 DR WPI: 2002-352536/38.
 DR N-PSDB: ABN67976.

Query Match: 87.0%; Score 1134; DB 21; Length 260;
Best Local Similarity: 87.2%; Pred. No. 1,6e-99;
Matches 225; Conservative 18; Mismatches 15; Indels 0; Gaps 0

QY 4 ACRSVKGLVAVTTGASGLGLATIERLVGQASAVLDDLENSGGEQAOKLNNVFAFA 63
Db 3 AFRSVKGLVAVTTGASGLGLATIAKRLVGQATVVLDDVPSGGEQAOKLIGSCIFAPA 62
QY 64 DVTSEKDVOTALAKGKFGFQDVAVNACGIAVASKTYNNKKGOTHTLEDFQFVLDVNL 123
Db 63 NTYSEKIEIQAALLTAKKEKFRIDVAVNACGIAVAIKTYHKKKKKHTLEDFQFVINVNI 122
QY 124 GFENVIRLVAGEMGONEPDGGQRCVITNTASVALEFGQVGAAYASAKSGIYGMTLPTA 183
Db 123 GFENVIRLVAGEMGONEPDGGQRCVITNTASVALEFGQVGAAYASAKSGIYGMTLPTA 182
QY 184 RDLAPIGIVMTIAGLFGTPTLTLPKVCNFIASQVPPPSRLGDPAEYAHVLQAIIEN 243
Db 183 RDLAPIGIVMTIAGLFGTPTLTLPKVCNFIASQVPPPSRLGDPAEYAHVLQAIIEN 242
QY 244 PFLNGEVIRLDGAIKMP 261
Db 243 PFLNGEVIRLDGAIKMP 260

RESULT 4
AB662988
ID ABB62988 standard; protein; 255 AA.
AC ABB62988;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 15756.
DE
XX Drosophila: developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
XX Drosophila melanogaster.
OS
XX MO200171042-A2.
XX
XX
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001MO-USO9231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI WPI: 2001-656860/75.
XX
XX N-PSDE; ABL07091.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX
XX Disclosure; SEQ ID NO 15756; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB1616176-AB1630511), expressed DNA
CC sequences (AB101840-AB1616175) and the encoded proteins
CC (AB57737-AB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.

[illegible]

Query	Subject	Score	Length	Positives	Identical	Similarity	Positives	Identical	Similarity
35	AA54LLDLPDPSNGEAAKRLGNVAFADYTSKDVQALALAKGFGHVDVAVNCAGI	87.1%	1136	20	227	99.6%	1136	20	227
1	AA54LLDLPDPSNGEAAKRLGNVAFADYTSKDVQALALAKGFGHVDVAVNCAGI	87.1%	1136	20	227	99.6%	1136	20	227
95	AA54SKTYNKKKQCTHTLEDFOVAVDYNLMGTFENYTRVAEDMONEPDDGGORGVTINFA	87.1%	1136	20	227	99.6%	1136	20	227
61	AA54SKTYNKKKQCTHTLEDFOVAVDYNLMGTFENYTRVAEDMONEPDDGGORGVTINFA	87.1%	1136	20	227	99.6%	1136	20	227
155	SVAAAFGGVGAQAAYASASGGVIGMTLPARDLAFIGIRVMTIAPGLFTGPIPLTSIPKVC	87.1%	1136	20	227	99.6%	1136	20	227
215	NFLASGVPPPSRLGDPAEYAHVYOAIIENPFLNEVIRLGGAIKRMQP	87.1%	1136	20	227	99.6%	1136	20	227
181	NFLASGVPPPSRLGDPAEYAHVYOAIIENPFLNEVIRLGGAIKRMQP	87.1%	1136	20	227	99.6%	1136	20	227

Key	Location/Qualifiers
Region	10..15
Region	/note="beta sheet region A"
Region	18..32
Region	/note="alpha helix region A"
Region	35..41
Region	/note="beta sheet region B"
Region	43..57
Region	/note="alpha helix region B"
Region	61..66
Region	/note="beta sheet region C"
Region	70..80
Region	/note="alpha helix region C"
Region	84..94
Region	/note="beta sheet region D"
Region	109..133
Region	/note="alpha helix region D"
Region	143..153
Region	/note="beta sheet region E"
Region	167..171
Region	/note="SCAD motif"
Region	185..186
Region	/note="alpha helix region A"
Region	190..196
Region	/note="beta sheet region F"
Region	204..218
Region	/note="alpha helix region F"
Region	247..252
Region	/note="beta sheet region G"

Sequence 260 AA;

84 266 20.4 285 22 AAU34648 E. coli cellular p
85 264.5 20.3 246 22 AAE02195 S. aureus NADPH-de
86 263 20.2 243 23 AAB54107 Lactococcus lactis
87 263 20.2 261 13 AAR27756 NAD affinity gluc
88 263 20.2 276 21 AAY54416 Secoisolaricresin
89 263 20.2 276 23 AAO21494 Secoisolaricresin
90 262.5 20.1 286 22 AAU36267 Pseudomonas aerugi
91 261 20.0 272 21 AAB10740 B. megaterium gluc
92 261 20.0 340 21 AAY54413 H. ghilani11/3. me
93 260 19.9 277 21 AAY54413 Secoisolaricresin
94 258.5 19.9 273 21 AAY54414 Secoisolaricresin
95 259 19.9 253 22 AAU36249 Pseudomonas aerugi
96 257.5 19.7 243 23 ABB47402 Listeria monocytog
97 257 19.7 247 16 AAR66291 Mycobacterium bovi
98 257 19.7 247 16 AAR63899 M. bovis p85 ORF1
99 257 19.7 247 18 AAM40809 M. bovis p85 opero
100 257 19.7 261 23 AAE20115 Lactobacillus rham

ALIGNMENTS

RESULT 1

ID AAW71471 standard; Protein: 261 AA.

AAW71471;

16-DEC-1998 (first entry)

ERAB protein.

Endoplasmic reticulum associated amyloid-beta peptide binding protein;

ERAB protein; amyloid-beta peptide inhibitor; demyelinating disease;

neurodegenerative disorder; therapy; Alzheimer's disease; schizophrenia;

Down's syndrome; Parkinson's disease; Huntington's disease;

multiple sclerosis.

Homo sapiens.

WO9840484-A1.

17-SEP-1998.

12-MAR-1998; 98WO-US04915.

12-MAR-1997; 97US-0815225.

(UYCO) UNIV COLUMBIA NEW YORK.

Stern DM, Yan SD;

WPI: 1998-531524/45.

N-PSDB: AAW60576.

Endoplasmic reticulum associated amyloid-beta peptide binding

Protein - Inhibitors of which can be used to treat neurodegenerative

disorders

Claim 2; Fig 1D; 53pp; English.

This sequence is the endoplasmic reticulum associated amyloid-beta peptide binding (ERAB) protein of the invention. The protein can be used in a method for evaluating the ability of an agent to inhibit binding of ERAB polypeptide to amyloid-beta peptide comprising: (a) incubating the ERAB polypeptide, the agent and amyloid-beta peptide under binding conditions; (b) determining the amount of amyloid-beta peptide bound to ERAB polypeptide; (c) comparison of the amount of binding with results from a control using no agent, so determining inhibition ability of the agent. The inhibitors identified by the method can be used to treat a neurodegenerative condition by administration of an agent that inhibits binding of an ERAB polypeptide to amyloid-beta peptide, particularly where the disease is Alzheimer's disease, Down's syndrome, Parkinson's

CC disease, Huntington's disease, schizophrenia, a demyelinating disease, or
CC multiple sclerosis. The inhibitors can also be used to treat other
CC neurodegenerative conditions including those associated with aging,
CC dentatorubral and pallidolysian atrophy, Machado-Joseph disease,
CC muscular dystrophy, senility, spinocerebellar ataxia type I, spinobulbar
CC muscular atrophy, stroke, and trauma.

SQ Sequence 261 AA;

Query Match 99.6%; Score 1299; DB 19; Length 261;

Best Local Similarity 99.6%; Pred. No. 3.5e-115;

Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MAACRSVKGVLAVITGGASGGLATAEKLVGGASAVLLDLPNSGGEQAARKLNQVF 60

1 APADVTSEKDVOTATLAKKFGKRVDAVNCAGIAVASKTYNLKQGTHTLDFORVLDV 120

61 APADVTSEKDVOTATLAKKFGKRVDAVNCAGIAVASKTYNLKQGTHTLDFORVLDV 120

121 NLMGTFNVIRLVAGENGQNEPDGQGVINTASVAAREGQCAAYASASGIGYKTL 180

121 NLMGTFNVIRLVAGENGQNEPDGQGVINTASVAAREGQCAAYASASGIGYKTL 180

181 PIARDLAPIGIRVMTIAPGLFGTPLTSLPEKVCNPLASQVPPSRGPAEYAHLYQAI 240

181 PIARDLAPIGIRVMTIAPGLFGTPLTSLPEKVCNPLASQVPPSRGPAEYAHLYQAI 240

241 IENPFLNGEVIRLDGAIRMOP 261

241 IENPFLNGEVIRLDGAIRMOP 261

RESULT 2

ID AAW67934 standard; Protein: 227 AA.

AAW67934;

25-MAR-1999 (first entry)

Fragment of human secreted protein encoded by gene 8.

Human; secreted protein; fusion protein; gene therapy; protein therapy;

diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

developmental abnormality; foetal deficiency; blood; allergy; renal;

immune system; asthma; lymphocytic disease; brain; hepatitis; lymphoma;

inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;

cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;

osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Homo sapiens.

WO9842738-A1.

01-OCT-1998.

19-MAR-1998; 98WO-US05311.

30-MAY-1997; 97US-0050937.

21-MAR-1997; 97US-0041276.

21-MAR-1997; 97US-0041277.

21-MAR-1997; 97US-0041281.

30-MAY-1997; 97US-0042344.

30-MAY-1997; 97US-0048069.

30-MAY-1997; 97US-0048094.

30-MAY-1997; 97US-0048095.

30-MAY-1997; 97US-0048096.

30-MAY-1997; 97US-0048099.

30-MAY-1997; 97US-0048131.

30-MAY-1997; 97US-0048135.

Thu Jun 26 06:55:09 2003

us-09-931-186-6.rag

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: June 23, 2003, 14:19:21 ; Search time 39.6667 Seconds

(without alignments)
876.767 Million cell updates/sec

Title: us-09-931-186-6

Perfect score: 1304

Sequence: 1 MAACRSVKGLVAVITGGAS.....ENPFLNGEIVRLDGAIRMP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :
1: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1980.DAT:*
2: /SID52/gcgdata/geneeqp-emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneeqp-emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneeqp-emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneeqp-emb1/AA1984.DAT:*
6: /SID52/gcgdata/geneeqp-emb1/AA1985.DAT:*
7: /SID52/gcgdata/geneeqp-emb1/AA1986.DAT:*
8: /SID52/gcgdata/geneeqp-emb1/AA1987.DAT:*
9: /SID52/gcgdata/geneeqp-emb1/AA1988.DAT:*
10: /SID52/gcgdata/geneeqp-emb1/AA1989.DAT:*
11: /SID52/gcgdata/geneeqp-emb1/AA1990.DAT:*
12: /SID52/gcgdata/geneeqp-emb1/AA1991.DAT:*
13: /SID52/gcgdata/geneeqp-emb1/AA1992.DAT:*
14: /SID52/gcgdata/geneeqp-emb1/AA1993.DAT:*
15: /SID52/gcgdata/geneeqp-emb1/AA1994.DAT:*
16: /SID52/gcgdata/geneeqp-emb1/AA1995.DAT:*
17: /SID52/gcgdata/geneeqp-emb1/AA1996.DAT:*
18: /SID52/gcgdata/geneeqp-emb1/AA1997.DAT:*
19: /SID52/gcgdata/geneeqp-emb1/AA1998.DAT:*
20: /SID52/gcgdata/geneeqp-emb1/AA1999.DAT:*
21: /SID52/gcgdata/geneeqp-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneeqp-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneeqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1399	99.6	261	19	AAW71471
2	1136	87.1	227	21	AAW67934
3	1134	87.0	260	21	AAI32239
4	913	70.0	255	18	ABW62988
5	664.5	51.0	388	12	AAW06513
6	366.5	28.1	244	23	ABP28011
7	356	27.3	243	23	ABP27345
8	331.5	25.4	243	19	AAW06706
9	331.5	25.4	243	21	AAW15706
10	331.5	25.4	243	22	AAU37767

11	331.5	25.4	243	22	AAU37988	Streptococcus pneu
12	330.5	25.3	243	22	AAW01032	CFE 35 protein seq
13	324.5	24.9	243	23	ABW54087	Lactococcus lactis
14	317	24.3	257	22	AAU28344	Novel human secret
15	314	24.1	237	22	AAW50255	Human dehydrogenas
16	312.5	24.0	241	22	AAW96397	Putative P. abyssal
17	312	23.9	237	22	AAU28156	Novel human secret
18	312	23.9	237	22	AAW19928	Human oxidoreducta
19	310.5	23.8	248	21	AAW54422	Amino acid sequenc
20	308.5	23.7	245	22	AAU35328	Enterococcus faeca
21	308.5	23.7	247	23	ABW48692	Listeria monocytog
22	301	23.1	247	21	AAW95746	Bacillus megaterium
23	297.5	22.8	267	22	AAW47459	Levodione reductas
24	295	22.6	263	23	ABP39667	Staphylococcus epi
25	294	22.5	262	22	AAW83032	S. epidermidis ope
26	292.5	22.4	303	23	AAW86337	G. suboxydans DSM
27	292.5	22.4	303	23	ABW92624	Herbicidally activ
28	291	22.3	315	17	AAW89323	Rape leaf beta-ket
29	291	22.3	315	17	AAW89322	Rape seed beta-ket
30	290.5	22.3	270	20	AAW41761	Human PRO474 prote
31	290.5	22.3	270	21	AAW44317	Human PRO474 (UNG5
32	290.5	22.3	270	21	AAW44056	Human PRO474 prote
33	290.5	22.3	270	22	AAU28108	Novel human secret
34	290.5	22.3	279	22	AAU18296	Human endocrine po
35	290.5	22.3	288	22	AAU28296	Novel human secret
36	289.5	22.2	244	21	AAW54421	Amino acid sequenc
37	289.5	22.2	244	21	AAW34533	Novel human secret
38	289.5	22.2	244	22	AAW10974	E. coli cellular p
39	288.5	22.1	246	10	AAW94157	Acetoacetyl CoA re
40	288.5	22.1	246	10	AAW94157	Acetyl-CoA reducta
41	288.5	22.1	246	14	AAW32192	Sequence encoded b
42	288.5	22.1	246	20	AAW43310	Acetoacetyl-CoA re
43	288.5	22.1	246	21	AAW54423	Amino acid sequenc
44	288.5	22.1	246	22	AAW71981	Rastonia eutropha
45	288.5	22.1	246	21	AAW44578	Xylylitol dehydrogen
46	286.5	22.0	246	16	AAW71324	Acetyl-CoA-reducta
47	285.5	21.9	246	21	AAW42558	Human ORF ORF222
48	285.5	21.9	246	22	AAW49773	Protein with acetyl
49	285.5	21.9	246	22	AAW54415	Secoisolactichresin
50	283.5	21.7	242	22	AAW59290	Prionolactichresin
51	282.5	21.7	242	23	ABW54214	Lactococcus lactis
52	282.5	21.7	242	23	ABW54214	Acetyl-CoA reducta
53	282.5	21.7	242	23	ABW54214	Herbicidally activ
54	280.5	21.5	246	12	AAW81644	S. epidermidis ope
55	279.5	21.4	246	14	AAW10679	Acetoacetyl CoA re
56	278.5	21.4	246	14	AAW47471	Acetoacetyl CoA re
57	278	21.3	243	23	ABW39586	Staphylococcus epi
58	277	21.2	244	22	AAW38499	Staphylococcus typhi c
59	276.5	21.2	244	22	AAW38499	Human AFP protein
60	276	21.2	244	22	AAW47522	(R)-2-octanol dehy
61	276	21.2	244	22	AAW47522	C glutamicum prote
62	274.5	21.1	244	22	AAW92682	Coriynobacterium gl
63	274	21.0	244	22	AAW92682	Herbicidally activ
64	273.5	21.0	244	22	AAW92682	Short-chain dehyd
65	273	20.9	244	20	AAW36959	Chlamydia trachoma
66	273	20.9	244	19	AAW38474	S. pneumoniae 3-ox
67	272.5	20.9	244	23	AAU77210	Consensus protein
68	272.5	20.9	244	23	ABW39980	Staphylococcus epi
69	272.5	20.9	244	23	ABW39980	Staphylococcus epi
70	271.5	20.8	244	16	AAW06488	Malee T52 sequence
71	269	20.6	244	21	AAW34193	Staphylococcus aur
72	268.5	20.6	244	21	ABW39552	Staphylococcus epi
73	268.5	20.6	244	21	AAW15707	Staphylococcus aur
74	268.5	20.6	244	22	AAW33965	Staphylococcus aur
75	268.5	20.6	244	22	AAW36530	Staphylococcus aur
76	268.5	20.6	244	22	AAW37210	Staphylococcus aur
77	267	20.5	246	22	AAW37507	Staphylococcus aur
78	266.5	20.4	244	23	ABW48207	Listeria monocytog
79	266.5	20.4	244	23	AAW35811	Haemophilus influe
80	266.5	20.4	244	23	AAW16940	Recombinant enzyme
81	266.5	20.4	244	21	AAW92509	Human OXR6-6. Hom
82	266.5	20.4	244	21	AAW35505	Escherichia coli p
83	266.5	20.4	244	21	AAW35505	Escherichia coli p
84	266.5	20.4	244	21	AAW35505	Arbidopsis thalia

Thu Jun 26 06:55:09 2003

Search completed: June 23, 2003, 14:35:41
Job time : 14.1667 secs

us-09-931-186-6.ra1

Page 12

```

; TYPE: PR
; ORGANISM: Staphylococcus aureus
US-09-572-810A-2
Db      65 KSNIDMLKAVIDHFGHIDIVVNSAGOSLSKTTD-----YVEQDNIWIDVNIQTILH 118
QY      128 VIRLVAGEMGQNEPDGQGGGVYIINTASVAAFEGQVQAAYSASKGIVGMLPIARDLA 187
      119 VLQATLPEYLKQ-----SSGHIINLASVSGFEPTKNNAVYGAATKAIHMTQSLKEELA 172
QY      188 PIGIRVMTIAPGLFETPL 205
      173 RTGVKATVISBPQMVDP 190

RESULT 23
US-09-238-481-2
; Sequence 2, Application US/09238481
; Patent No. 6110704
; GENERAL INFORMATION:
; APPLICANT: Huang, Jiansheng
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Fabg
; FILE REFERENCE: GMI0192
; CURRENT APPLICATION NUMBER: US/09/238,481
; CURRENT FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 246
; TYPE: PR
; ORGANISM: Staphylococcus aureus
US-09-238-481-2
Query Match      20.6%; Score 268.5; DB 3; Length 246;
Best Local Similarity 28.7%; Pred. No. 6.8e-22;
Matches 73; Conservative 57; Mismatches 103; Indels 21; Gaps 6;

QY      13 AVITGASGLGLTAERLVGQASAVLLDLPNSGGEAQA-----KRLGNVVFAPADYTS 67
      7 ALVTGASRGIGRSIALQIAEEGYV-VAVNYAGSKKAEVVEETKAGVDSFAIQANVAD 65
QY      68 EKDVOTATLALAKGKRGVAVNAGIAVASKTYNLKKQTHLEDFQVLDVNLGTFN 127
      66 ADEVKAMIKKEYVSGFSDVLVNNAGITRDNLKMRKE-----QEMDVIDTNLKGTFN 119
Db      128 VIRLVAGEMGQNEPDGQGGGVYIINTASVAAFEGQVQAAYSASKGIVGMLPIARDLA 187
QY      120 CIQKATPQMLRQ-----RSGAIINLSVVGAVNPGQANVATKAGVIGLTKSARELA 173
      188 PIGIRVMTIAPGLFETPLTSLPEKVCNPLASQVFPFSRLGDPAEVAHLVQAILEN--PF 245
      174 SRGITVNAVAPGFIVSDMTDALSDELKQMLTQIPL-ARFGQDDIDIANVAFSLADSKAKY 232
QY      246 LNGEVIRLDGAIRM 259
      233 ITGQTIHVNGMYM 246

Db      233 ITGQTIHVNGMYM 246

RESULT 24
US-09-572-810A-2
; Sequence 2, Application US/09572810A
; Patent No. 6365387
; GENERAL INFORMATION:
; APPLICANT: Huang, Jiansheng
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Fabg
; FILE REFERENCE: GMI0192
; CURRENT APPLICATION NUMBER: US/09/572,810A
; CURRENT FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 09/238,481
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 246

; TYPE: PR
; ORGANISM: Staphylococcus aureus
US-09-572-810A-2
Query Match      20.6%; Score 268.5; DB 4; Length 246;
Best Local Similarity 30.9%; Pred. No. 1.4e-21;
Matches 82; Conservative 39; Mismatches 116; Indels 28; Gaps 8;

QY      10 GLVAVITGASGLGLTAERLVGQASAVLLDLPNSGGEAQAQKL--GNNVFAPADYTS 66
      6 KVAVITGGAAGKRGIOSELVYASEQAVAVDVNEQGRATADAIASGQVAVNYMLDVS 65
QY      67 SEKDVOATLALAKGKRGVAVNAGIAVASKTYNLKKQTHLE--DFQVLDVNLG 124
      66 DESEVELVSDIAKRGAGALVAVNAGVADK-----PTHEIDERDLDVLSVDVKG 118
Db      125 TFNVIRLVAGEMGQNEPDGQGGGVYIINTASVAAFEGQVQAAYSASKGIVGMLPIAR 184
      119 VFEFTKRCIPYKQ---AGG--GAIYNFASIVGIVSOLPLHYHAKGAVVALLTXQDAV 172
QY      185 DIAPIGIRVMTIAPGLFETPLTSLPEK-----VCNPLASQVFPFSRLGDPAEV--AH 235
      173 TYGSPNIRVAVAPGILITPLVKELSRGQDGLDGTITKLGAKHPL-GRVGTPEEVAAT 231
QY      236 LVQAIENPFLNGEVIRLDGAIRMQ 260
      232 LFLASEASFTIGAVLPVQDGYTAQ 256

; TYPE: PR
; ORGANISM: Staphylococcus aureus
US-09-504-358-14
Query Match      20.4%; Score 266; DB 4; Length 256;
Best Local Similarity 30.9%; Pred. No. 1.4e-21;
Matches 82; Conservative 39; Mismatches 116; Indels 28; Gaps 8;

QY      10 GLVAVITGASGLGLTAERLVGQASAVLLDLPNSGGEAQAQKL--GNNVFAPADYTS 66
      6 KVAVITGGAAGKRGIOSELVYASEQAVAVDVNEQGRATADAIASGQVAVNYMLDVS 65
QY      67 SEKDVOATLALAKGKRGVAVNAGIAVASKTYNLKKQTHLE--DFQVLDVNLG 124
      66 DESEVELVSDIAKRGAGALVAVNAGVADK-----PTHEIDERDLDVLSVDVKG 118
Db      125 TFNVIRLVAGEMGQNEPDGQGGGVYIINTASVAAFEGQVQAAYSASKGIVGMLPIAR 184
      119 VFEFTKRCIPYKQ---AGG--GAIYNFASIVGIVSOLPLHYHAKGAVVALLTXQDAV 172
QY      185 DIAPIGIRVMTIAPGLFETPLTSLPEK-----VCNPLASQVFPFSRLGDPAEV--AH 235
      173 TYGSPNIRVAVAPGILITPLVKELSRGQDGLDGTITKLGAKHPL-GRVGTPEEVAAT 231
QY      236 LVQAIENPFLNGEVIRLDGAIRMQ 260
      232 LFLASEASFTIGAVLPVQDGYTAQ 256
```


Thu Jun 26 06:55:09 2003

us-09-931-186-6.ral

Page 9

1 FILING DATE: 13-AUG-1990
2 APPLICATION NUMBER: 67,695
3 FILING DATE: 29-JUN-1987
4 SEQ ID NO:4
5 LENGTH: 273
6 5512669-4

Query Match 21.7%; Score 282.5; DB 6; Length 273;
Best Local Similarity 31.5%; Pred. No. 2,2e-23;
Matches 90; Conservative 42; Mismatches 91; Indels 63; Gaps 11;

QY 12 VAVITGASGLALAEKLVGOGASAVLDDLPNSGEGQAKKLNINVFAPA-----63
DB 4 VALVVGSGRGID-----NAISIAKAAQYKVAASVAGDDAKPFKAETGIAY 51
QY 64 ---DVTSEKDVOTALALAKGKFRVDVAVNCGIIVASKTYNLKKGOTHTLEDFOFVL 118
DB 52 YKWDVSYEACVEGIAKYEADIGPIDVLNNAGIT-----KDAHFHKITPDQWNAVY 103
QY 119 DVNLAKGTFRVY-----RLV-----AGEMQ-NEPDQGGOR-----GVYIN 152
DB 104 MNTLGLFNMTHPVMSGMRSEFRIVNMISSINGQGMQANSVMSGMDRSEFRIVN 163
QY 153 TASVAFEGOVGAOYASAKSGIYVMTLPIDADLPAGIRVMTIAPGLFTPLTSPDK 212
DB 164 ISSINGQGMQOQANYSAAKAGDGLFTALAGAKITVNAICPGYIGTEMVRAIPER 223
QY 213 VCN-FLASQVPPPSRLGDPAEYAHV--QAIENPFLNGEVIRLDG 255
DB 224 VNERIIRIPQIPV-GRIGEPDEIARIIVFLASDEAGITGSIISANG 268

RESULT 18

US-09-134-001C-4431
Sequence 4431, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: CTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4431
LENGTH: 274
TYPE: PAT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4431

Query Match 21.4%; Score 278.5; DB 4; Length 274;
Best Local Similarity 31.7%; Pred. No. 6,2e-23;
Matches 85; Conservative 45; Mismatches 93; Indels 45; Gaps 8;

QY 12 VAVITGASGLALAEKLVGOGASAVLDDLP-----NSGEGQAKKLNINVF 60
DB 10 IAVITGASGLGASAVLALAEAGAVLALDISDQLEETVQSIINDGKATAYRV-----63
QY 61 APADVTSEKDVOTALALAKGKFRVDVAVNCGIIVASKTYNLKKGOTHTLEDFOFVL 118
DB 64 ---DISDKQYKQSEKLAQEFQVAVLNNAGVNGA-----GRHEYPVEYFDKIM 113
QY 119 DVNLAKGTFRVYVAVNCGEONEPDQGGORGVYINTASVAFEGOVGAOYASAKSGIYGM 178
DB 114 AVDMGSLTFLYKFL-----PLMKOGSITINASTSGAADIYRSYGIAAKAGVYINF 166
QY 179 TLPIARDLAPIGIRVMTIAPGLFTPL-----TSLPKVCNFTLASQ--VPPPSRLGDP 231
DB 167 TKSIAIEYGRNIRANALAPGTIERPLVDNLAGTSDDEAGOTFRNCRKMTVPLIGRLTDPD 226

QY 232 EYAHVQ--AIENPFLNGEVIRLDGAI 257
DB 227 EVGKLVAFLASDDSPFITGETIRIDGCV 254

RESULT 19

US-08-858-207A-270
Sequence 270, Application US/08858207A
Patent No. 6348328

GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 270:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6348328e
US-08-858-207A-270

Query Match 20.9%; Score 273; DB 4; Length 186;
Best Local Similarity 39.3%; Pred. No. 1,4e-22;
Matches 75; Conservative 23; Mismatches 71; Indels 22; Gaps 5;

QY 15 ITGASGLALAEKLVGOGASAVLDDLPNSGE-----AQAKKLNINVPADVTSE 68
DB 10 ITGSSRGIGLALAHKFRQAGANIVL-----NSRGAISPELLAESNGIKYVPPISGVSDP 65
QY 69 KDVOFALALAKGKFRVDVAVNCGIIVASKTYNLKKGOTHTLEDFOFVLVDVNLGTFVY 128
DB 66 ADARFMIDQAIHAEIGSDVVLVNNAGI--TODTLMELK-----TEADFEKVLKYNLTGAFNM 119
QY 129 IRLVAGMGONEPDQGGORGVYINTASVAFEGOVGAOYASAKSGIYVGTLPIDADLP 188
DB 120 TQSYLV-----KPMKARBAEAIINMSSVGLMGINIGQANTAAKAGLIGTTSKVAAREVAS 173
QY 189 IGIRVMTIAPG 199
DB 174 RNIRVNIAPG 184

APPLICATION NUMBER: 08/562,114
FILING DATE: 22-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/375,962
FILING DATE: 20-January-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 10-June-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 628097man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5372.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
US-08-729-594A-13

Query Match 21.9%; Score 285.5; DB 4; Length 244;
Best Local Similarity 29.6%; Pred. No. 8.5e-24;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;

QY 9 KGLVAVITGGASGLGATAEKLVGOGASAVYLDLPNSGGEAKKLGNNVFAADVTSE 68
DB 4 EKKIALVTGASRGIGRAIAETLAARGKVIATSENQAISDYLGANGKGLMANTDP 63
QY 69 KDVOITALAKGKFGKRVDAVAVNCAGIAVASKTYNLKGGOTHTLDFORVLDVNLKGFNV 128
DB 64 ASIESVLEKRAEFGEVDILVNNAGITRDNLKMRKD-----EEMNDIETNLSVFL 117
QY 129 IRLVAGMGONEPDGGRGVIIINTASVAAREGOVGAAYASAKSGIVGMLPIARDLAP 188
DB 118 SKAVRAMMKK-----RHGRITITGSVGTMGNGGQANYAAKAGLIGFSKSLAREVAS 171
QY 189 IGRVMTIADLGFPTLLTSLPEKVCNFLASQVPEPRLGDPAEYAHVQ--AIENPFL 246
DB 172 RGIIVNVVAPGFIETDTRALSDORAGIIVAP-AGRLGAGQEIANAVAFASDEAYI 230
QY 247 NGEVIRLDGAIRM 259
DB 231 TGETLVHNGMYM 243

RESULT 16
US-08-937-993-13
Sequence 13, Application US/08937993
Patent No. 6399344

GENERAL INFORMATION:
APPLICANT: Eriksson, Ulf; Simon, Andras; Romert, Anna
TITLE OF INVENTION: ISOLATED PROTEINS HAVING CIS-R
TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,993

FILING DATE: September 26, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/729,594
FILING DATE: 11-October-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/562,114
FILING DATE: 22-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6399344man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
US-08-937-993-13

Query Match 21.9%; Score 285.5; DB 4; Length 244;
Best Local Similarity 29.6%; Pred. No. 8.5e-24;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;

QY 9 KGLVAVITGGASGLGATAEKLVGOGASAVYLDLPNSGGEAKKLGNNVFAADVTSE 68
DB 4 EKKIALVTGASRGIGRAIAETLAARGKVIATSENQAISDYLGANGKGLMANTDP 63
QY 69 KDVOITALAKGKFGKRVDAVAVNCAGIAVASKTYNLKGGOTHTLDFORVLDVNLKGFNV 128
DB 64 ASIESVLEKRAEFGEVDILVNNAGITRDNLKMRKD-----EEMNDIETNLSVFL 117
QY 129 IRLVAGMGONEPDGGRGVIIINTASVAAREGOVGAAYASAKSGIVGMLPIARDLAP 188
DB 118 SKAVRAMMKK-----RHGRITITGSVGTMGNGGQANYAAKAGLIGFSKSLAREVAS 171
QY 189 IGRVMTIADLGFPTLLTSLPEKVCNFLASQVPEPRLGDPAEYAHVQ--AIENPFL 246
DB 172 RGIIVNVVAPGFIETDTRALSDORAGIIVAP-AGRLGAGQEIANAVAFASDEAYI 230
QY 247 NGEVIRLDGAIRM 259
DB 231 TGETLVHNGMYM 243

RESULT 17
5512669-4
Patent No. 5512669
APPLICANT: PROPLES, OLIVER P.; STINSKEY, ANTHONY J.
TITLE OF INVENTION: GENE ENCODING BACTERIAL ACETOACETYL-COA
REDUCTASE
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,667
FILING DATE: 29-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 124,570
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 944,488
FILING DATE: 03-NOV-1992
APPLICATION NUMBER: 566,535

```

1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: 08/258,418
3 FILING DATE: 6-October-1994
4 ATTORNEY/AGENT INFORMATION:
5 NAME: Pasqualini, Patricia A.
6 REGISTRATION NUMBER: 34,894
7 REFERENCE/DOCKET NUMBER: L0D 5372.1 CIP
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: (212) 688-9200
10 TELEFAX: (212) 838-3884
11 INFORMATION FOR SEQ ID NO: 13:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 244 amino acids
14 TYPE: amino acid
15 STRANDEDNESS: single
16 TOPOLOGY: linear
17 MOLECULE TYPE: protein
18 FEATURE:
19 NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]
20 NAME/KEY: reductase (FabG)
21 OS-08-373-962b-13

```

Query Match	21.98;	Score 285.5;	DB 1;	Length 244;
Best Local Similarity	29.68;	Pred. No. 8.5e-24;		
Matches	75;	Conservative	50;	Mismatches 113;
			Indels	15;
			Gaps	4;

QY		9	KGVAVITGSGAGSLGATAAERLVGGASAVLLDLPNNGGGAOKKGINNVVFPADPTESE	68
Dd		4	EKGIALVTGASGIGIAIETLTAARGGVISTATSENGAQAIIDYGANCKGLMLNTDP	63
QY		69	KDKQTALATARKCFGRVDVAVNCAGIVASTVYLKKGGTHLEDEORVLDVNLMTGFNV	128
Dd		64	AASIESYLEKIRAFEGFSDVLVNNAGITHDNLMMKP-----EENMDIIENLSVFEL	117
QY		129	IRLYAEMSCONEDGGGORGVIINTASYAAEEGVOGAAYSASAKGIVGTPLDIANDLP	168
Dd		118	SKRVMAAMMK-----RGRITTIIGSVYGMINGMGOGANYAAKAGLTGFSKLAREVAS	171
QY		189	IGIRVWTINAPGLFGPTPLTSLPEKYCNLASQVFFPSRLDDPAFYAHLYO-AITINPFL	246
Dd		172	RGLTVVAVPAGFTIEDMRALSDDORAGILAOVP-AGRLLGACBIANAFAFLDSAEAYI	230
QY		247	NGEVIRLDGAIRM	259
Dd		231	TGETLHVNGGMTN	243

RESULT 14
 US-08-562-114B-13
 Sequence 13, Application US/08562114B
 Patent No. 5972646
 GENERAL INFORMATION:
 APPLICANT: ERIKSSON ET AL.
 TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH CODES FOR A
 TITLE OF INVENTION: 32 KDA PROTEIN HAVING 11-CIS RETINOL HYDROGENASE
 TITLE OF INVENTION: ACTIVITY, AND WHICH ASSOCIATES WITH P63, A
 TITLE OF INVENTION: PORTION OF A RETINOL BINDING PROTEIN RECEPTOR
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felle & Lynch
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect 5.1 and ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/562,114B
 FILING DATE: 22-No. 5972646member-1995
 CLASSIFICATION: 435

```

1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: 08/375,962
3 FILING DATE: 20-January-1995
4 ATTORNEY/AGENT INFORMATION:
5 NAME: Kohli, Vineet
6 REGISTRATION NUMBER: 37,003
7 REFERENCE/DOCKET NUMBER: LUD 5372.2 CIP
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: (212) 688-9200
10 TELEFAX: (212) 638-3884
11 INFORMATION FOR SEQ ID NO: 13:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 244 amino acids
14 TYPE: amino acid
15 TOPOLOGY: linear
16 MOLECULE TYPE: protein
17 FEATURE:
18 NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
19 NAME/KEY:
20 US-08-562-114B-13

```

Query Match	21.9%	Score 285.5	DB 2	Length 244
Best Local Similarity	29.6%	Prod. No. 8.5e-24		
Matches 75, Conservative	50	Mismatches 113	Indels 15	Gaps 4

QY	9	KGLAAVITGGSSGIGLTAERTLVGQGSAAVLLDPSNGSGEAOAKLGNVVFAADVTSE	68
Db	4	EKGALVYTGASRSGRGRAIAETRLAARGGVISTATSEKGAQXISPLYLGANGKGLMANTDP	63
QY	69	KDVOTATALAKGKGFRAVDVAVNCAGIAVASKTYMLKKGFHTLDFQFVRLDVMNGTFNV	128
Db	64	ASIESVLEKRIAEFGVEDILVNNGAGITPDLNLMKKD-----EDWMDIETNLSVEFL	117
QY	129	IRLVAEGMGOREPDGGGGRVYIINTASAAPEGGVQGAASASGSGIVGMLPLPARGLP	188
Db	118	SKAAMRAMMK-----RHGRILITGVSVMGNGGQGANVAAAKAGLIGPSKLAREVAS	171
QY	189	IGIIVMTLAPLCEGTPLLITSLPEKVCNFLASQVFPSSLPGRABAYHLYQ--AIIENPFL	246
Db	172	RGIIVNVNVAPEFIETDMTRALSDQORAGIILAQV--AGRLGSAQELIANVATLASDEAYI	230
QY	247	NGEYIRLDGAIIRM	259
Db	231	TGETLHVNGGMYM	243

```

1      RESULT 15
2      US-08-729-594A-13
3      ; Sequence 13, Application US/08729594A
4      ; Patent No. 6280997
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Eriksson, Ulf; Simon, Andras; Romert, Anna
7      ; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH
8      ; TITLE OF INVENTION: CODES FOR A 32 KDA PROTEIN HAVING 11-CIS RETINOL DEHYD
9      ; TITLE OF INVENTION: ACTIVITY, AND WHICH ASSOCIATES WITH P53, A PORTION OF
10     ; TITLE OF INVENTION: RETINOL BINDING PROTEIN RECEPTOR
11     ; NUMBER OF SEQUENCES: 41
12     ; CORRESPONDENCE ADDRESS:
13     ; ADDRESSEE: Felfe & Lynch
14     ; STREET: 805 Third Avenue
15     ; CITY: New York City
16     ; STATE: New York
17     ; ZIP: 10022
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
20     ; COMPUTER: IBM
21     ; OPERATING SYSTEM: PC-DOS
22     ; SOFTWARE: Wordperfect
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/08/729,594A
25     ; FILING DATE: 11-October-1996
26     ; CLASSIFICATION: 435
27     ; PRIOR APPLICATION DATA:

```


Thu Jun 26 06:55:09 2003

us-09-931-186-6.ra1

Page 4

ADDRESS: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-440-856A-4
Query Match 23.4%; Score 304.5; DB 1; Length 333;
Best Local Similarity 32.9%; Pred. No. 1e-25;
Matches 93; Conservative 46; Mismatches 105; Indels 39; Gaps 5;
QY 6 RSVKGLVAVITGASGGLATAEKLVGGASAVILDPNSGGEQAOKLGNVYFADY 65
DB 50 KRLBEKVAIVTGGARGIDEALVFLVHRGAKVVIADIDDAAGELAAALGPHGVFVCDV 109
QY 66 TSEKVOFALALAKGKFRVAVNACAGIAVASKTYNLKKGOTHTLDFQVLDVNLGTF 125
DB 110 SYEEVERAVERAARVARDLVLCNNAGV-LGRQTPRAKSLTSPDAGEFDEVLKVNLA 168
QY 126 FNVITLVAGEKQNEPDGQGVYINTASVAAEFGVGAAYASAGGIYGTLPPLARD 185
DB 169 ALGKHAALAMTOR-----RAGSLISVAVAGVLGGLPHAYASKHAIVGLTKNAKE 222
QY 186 LAPIGIRVMTAPGLFGTPLL-----TSLP-----EKVC 214
DB 223 LGAGIRVNCISFPGVATPMLINARQGHDASTADADADIDDIIVASDQEVKEMEYV 282
QY 215 NFASQVFPRLGDPAAVLAHVQAIENPFLNGEVIRLDGAI 257
DB 283 RGLATLKGATLRPDIAE-AALFLASDSDRYISGHNLVVDGV 324
RESULT 7
US-08-815-225-4
Sequence 4, Application US/08815225
Patent No. 6268479
GENERAL INFORMATION:
APPLICANT: Stern, David M.
TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE
TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING
TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,225
FILING DATE: 12-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/55209
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-815-225-4
Query Match 22.9%; Score 299; DB 4; Length 255;
Best Local Similarity 33.6%; Pred. No. 2.8e-25;
Matches 85; Conservative 47; Mismatches 101; Indels 20; Gaps 8;
QY 8 VVGLVAVITGASGGLATAEKLVGGASAVILDPNSGGEQAOKLGNVYFADY 67
DB 4 LSKGTVIITGGARGIAEAARQAVAAAGARVAVADVLDEGATTAELDPAARYQHLDTI 63
QY 68 EKDVOFALALAKGKFRVAVNACAGIAVASKTYNLKKGOTHTLDFQVLDVNLGTF 127
DB 64 EEDMOWAVAYAKREFSVGLVNNAGISTGMEL-----ETESVERFRVVDINTLGVFI 117
QY 128 FNVITLVAGEKQNEPDGQGVYINTASVAAEFGVGAAYASAGGIYGTLPPLARD 187
DB 118 GAKTVIPAM---KDAKG--GSLVINISSAAGLGLTSSYASKVGWGLSKLAIVELG 171
QY 188 PIGIRVMTAPGLFGTPLL--TSLPEKVCNFLASQVFPSPRLG-DPAEYAHVQAIIIE-- 242
DB 172 TDRIKRVASHPKATYTPMAEIGIRGEGNY--PNTPM-GRVNGEGELAGAVVLLSDT 228
QY 243 NPFLNGEVIRLDG 255
DB 229 SSYVTGAELAVDG 241
RESULT 8
US-09-134-001C-4512
Sequence 4512, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4512
LENGTH: 263
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4512

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 28865-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
US-09-347-878-50

Query Match 99.6%; Score 1299; DB 4; Length 261;
Best Local Similarity 99.6%; Pred. No. 4.2e-137;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLGATERTLVGGASAVLLDIPNSGGEAAKLGNNVVF 60
DB 1 MAACRSYKGLVAVITGASGLGATERTLVGGASAVLLDIPNSGGEAAKLGNNVVF 60
QY 61 APADVTSEKDVQATLALAKGFRGVDAVAVNCAGIAVASKTYNLKGGTHLEDFORVLDV 120
DB 61 APADVTSEKDVQATLALAKGFRGVDAVAVNCAGIAVASKTYNLKGGTHLEDFORVLDV 120
QY 121 NLMGTFNVIRLVAGEKGNEDDGGQGVIIINTASVAEPGQGAAYASAKGIGVMTL 180
DB 121 NLMGTFNVIRLVAGEKGNEDDGGQGVIIINTASVAEPGQGAAYASAKGIGVMTL 180
QY 181 PIADLAPIGIRVMTIAPGLFETPLTSLPEKVCNFIASQVFPFSRIGDAEYAHVQAI 240
DB 181 PIADLAPIGIRVMTIAPGLFETPLTSLPEKVCNFIASQVFPFSRIGDAEYAHVQAI 240
QY 241 IENPFLNGEVRILDGAIKRMOP 261
DB 241 IENPFLNGEVRILDGAIKRMOP 261

RESULT 4
US-08-980-832-41
Sequence 41, Application US/08980832B
Patent No. 6291204
GENERAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Tsyanikov, Yuri
TITLE OF INVENTION: Improved Fermentative Carotenoid Production
FILE REFERENCE: Improved Fermentative Carotenoid
CURRENT APPLICATION NUMBER: US/08/980,832B
CURRENT FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41
LENGTH: 388
TYPE: PRT
ORGANISM: Flavobacterium sp. R1534
US-08-980-832-41

Query Match 51.0%; Score 664.5; DB 4; Length 388;
Best Local Similarity 55.5%; Pred. No. 7.2e-66;
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VKGLVAVITGASGLGATERTLVGGASAVLLDIPNSGGEAAKLGNNVVFAPADVT 67
DB 143 IEGRFVVTGASGLGASARMLAOGAKVYLADL-----AEPDAPEGAVHAACDVTD 196
QY 68 EKDVOTATLAKGFRGVDAVAVNCAGIAVASKTYNLKGGTHLEDFORVLDVNLGTFN 127
DB 197 ATAAATATATADRGRDLGVNCGIAPAEEM--LGNDGPRIGLDSFARAVTINLGSFN 254
QY 128 VIRLVAGEKGNEDDGGQGVIIINTASVAEPGQGAAYASAKGIGVMTLPIARDLA 187
DB 255 MARLAEMARNEPVR-GERGVIVTASTIAODGQIGGVAVYASAKGAVAGMTLPMARDLA 313
QY 186 PIGIVMTIAPGLFETPLTSLPEKVCNFIASQVFPFSRIGDAEYAHVQAIENPFLN 247

DB 314 RHGIRVMTIAPGLFETPLTSLPEKVCNFIASQVFPFSRIGDAEYAHVQAIENPFLN 373
QY 248 GEVIRLDGAIKRMOP 261
DB 374 GEVIRLDGAIKRMOP 387

RESULT 5
US-09-239-052-2
Sequence 2, Application US/09239052
Patent No. 6346395
GENERAL INFORMATION:
APPLICANT: Holmes, David J.
APPLICANT: Zhong, Yixi
APPLICANT: Debouck, Christine
APPLICANT: Jaworski, Deborah D.
APPLICANT: Wang, Min
APPLICANT: Warren, Richard L.
APPLICANT: Kosmatka, Anna L.
APPLICANT: McDevitt, Damien
APPLICANT: Ingraham, Karen A.
APPLICANT: Chalker, Allison F.
APPLICANT: So, Chi Young
APPLICANT: Wallis, Nicola G.
APPLICANT: Pearson, Stewart C.
TITLE OF INVENTION: Fabg
FILE REFERENCE: GM10191
CURRENT APPLICATION NUMBER: US/09/239,052
CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 243
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-239-052-2

Query Match 25.4%; Score 331.5; DB 4; Length 243;
Best Local Similarity 35.5%; Pred. No. 6e-29;
Matches 89; Conservative 36; Mismatches 103; Indels 23; Gaps 6;

QY 15 ITGASGLGATERTLVGGASAVLLDIPNSGGE-----AAKKGNNVVFAPADVTSE 68
DB 10 ITGSSRSIGLAIHAKFQAAGANIVL---NSRGAISELLAEFSNYGKIVPISGVDF 65
QY 69 KDVTATLAKGFRGVDAVAVNCAGIAVASKTYNLKGGTHLEDFORVLDVNLGTFN 128
DB 66 ADARMTIDQAIIEIGSDVAVNNAGI--TQDTMLCK---TADFEKVLKVLTAFTN 119
QY 129 IRLVAGEKGNEDDGGQGVIIINTASVAEPGQGAAYASAKGIGVMTLPIARDLA 188
DB 120 TQSVL-----KPMKREGAIIINMSVGLMIGNIGANAAKAGLIGFTKSVAREVAS 173
QY 189 IGRVMTIAPGLFETPLTSLPEKVCNFIASQVFPFSRIGDAEYAHVQAIENPFLN 248
DB 174 RNIIVNVIAPGMIESTDITSLDKIKETLAQIPM-KEFGQABQVADLTVELAGODYLIG 232
QY 249 EVIRLDGAIKRM 259
DB 233 QVIAIDGGLSM 243

RESULT 6
US-08-440-856A-4
Sequence 4, Application US/08440856A
Patent No. 5750873
GENERAL INFORMATION:
APPLICANT: DELAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:

ALIGNMENTS

RESULT 1

US-08-815-225-2
; Sequence 2, Application US/08815225

; Patent No. 6268479

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/815,225

; FILING DATE: 12-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/55209

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 391-0525

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 261 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-815-225-2

; Query Match

; Best Local Similarity 99.6%; Score 1299; DB 4; Length 261;

; Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

US-08-815-225-3
; Sequence 3, Application US/08815225

; Patent No. 6268479

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/815,225

; FILING DATE: 12-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/55209

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 391-0525

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 261 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-815-225-3

; Query Match

; Best Local Similarity 99.6%; Score 1299; DB 4; Length 261;

; Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

US-09-347-878-50
; Sequence 50, Application US/09347878C

; Patent No. 6376210

; GENERAL INFORMATION:

; APPLICANT: Yuan, Chong

; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/347,878

; FILING DATE: 12-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/55209

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 391-0525

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 261 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-09-347-878-50

; Query Match

; Best Local Similarity 99.6%; Score 1299; DB 4; Length 261;

; Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

; Qy

; Db

Thu Jun 26 06:55:09 2003

us-09-931-186-6.rat

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 14:24:27 ; Search time 12.1667 Seconds

(without alignments)
631.182 Million cell updates/sec

Title: US-09-931-186-6

Sequence: 1 MAACRSYKGLAVITGAS.....ENPLNGEVLRLDGAIRMQP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 100 summaries

Database :

- 1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/PCITUS.COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/Dackfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1299	99.6	261	4	US-08-815-225-2
2	1299	99.6	261	4	US-08-815-225-3
3	1299	99.6	261	4	US-09-347-878-50
4	664.5	51.0	388	4	US-08-980-832-41
5	331.5	25.4	243	4	US-09-239-052-2
6	304.5	23.4	333	1	US-08-440-856A-4
7	299	22.9	255	4	US-08-815-225-4
8	295	22.6	263	4	US-09-134-001C-4512
9	292.5	22.4	262	4	US-09-363-189B-6
10	291	22.3	315	3	US-08-793-035-9
11	291	22.3	315	3	US-08-793-035-10
12	288.5	22.1	246	6	5229279-7
13	285.5	21.9	244	1	US-08-375-962B-13
14	285.5	21.9	244	2	US-08-562-114B-13
15	285.5	21.9	244	4	US-08-729-594A-13
16	285.5	21.9	244	4	US-08-937-993-13
17	282.5	21.7	273	6	5512669-4
18	278.5	21.4	274	4	US-09-134-001C-4431
19	273	20.9	186	4	US-08-858-207A-270
20	272.5	20.9	249	4	US-09-134-001C-4825
21	272.5	20.9	337	1	US-08-440-856A-3
22	269	20.6	231	4	US-09-134-001C-4397
23	268.5	20.6	246	3	US-09-238-481-2
24	268.5	20.6	246	4	US-09-572-810A-14
25	266	20.4	246	4	US-09-504-338-14
26	266	20.4	256	4	US-09-954-314-14
27	257	19.7	247	1	US-08-241-766-13

28	255.5	19.6	263	6	5229279-4
29	254	19.5	261	4	US-09-468-738A-29
30	254	19.5	261	4	US-09-940-019-29
31	253.5	19.4	252	3	US-08-822-322-8
32	253.5	19.4	252	4	US-09-466-109-8
33	253.5	19.4	252	4	US-09-134-001C-3562
34	252.5	19.4	263	4	US-09-134-001C-3505
35	247	18.9	359	1	US-08-440-856A-7
36	245	18.8	256	1	US-08-594-808B-7
37	243	18.6	271	2	US-07-637-665-2
38	242	18.6	258	4	US-09-504-358-12
39	242	18.6	258	4	US-09-954-314-12
40	229.5	17.6	251	3	US-08-822-322-9
41	229.5	17.6	251	4	US-09-466-109-9
42	228	17.5	283	4	US-09-367-012-1
43	228	17.5	283	4	US-09-777-157A-1
44	228	17.5	292	3	US-09-109-205-2
45	228	17.5	292	4	US-09-443-184-58
46	215	16.5	267	4	US-08-134-001C-5042
47	211	16.2	283	4	US-09-134-001C-5346
48	207	15.9	313	4	US-09-413-814-9
49	206	15.8	290	4	US-09-134-001C-4339
50	200	15.3	244	2	US-09-090-567-2
51	191	14.6	248	4	US-09-385-028-11
52	186.5	14.3	318	4	US-08-729-594A-39
53	186.5	14.3	318	4	US-08-937-993-13
54	185.5	14.2	295	3	US-09-002-298-5
55	183.5	14.1	272	4	US-09-134-001C-2864
56	183.5	14.1	292	4	US-09-468-738A-2
57	183.5	14.1	292	4	US-09-940-019-2
58	183.5	14.1	296	4	US-09-468-738A-23
59	183.5	14.1	296	4	US-09-940-019-23
60	183.5	14.1	318	2	US-08-562-114B-15
61	183.5	14.1	318	3	US-08-109-205-17
62	183.5	14.1	318	4	US-08-729-594A-15
63	183.5	14.1	318	4	US-08-860-427-1
64	183.5	14.1	318	4	US-09-306-538B-1
65	183.5	14.1	318	4	US-08-937-993-15
66	182.5	14.0	295	4	US-09-134-001C-4059
67	182.5	14.0	318	1	US-08-375-962B-14
68	182.5	14.0	318	4	US-08-940-424-3
69	182	14.0	244	1	US-08-762-129-4
70	182	14.0	244	1	US-08-762-129-4
71	182	14.0	295	4	US-09-026-462B-2
72	177	13.6	301	4	US-09-288-143-38
73	177	13.6	318	4	US-08-729-594A-38
74	177	13.6	318	4	US-08-937-993-38
75	175	13.4	303	3	US-09-002-298-1
76	172	13.2	257	4	US-09-287-097-2
77	169.5	13.0	317	4	US-08-729-584A-37
78	169.5	13.0	317	4	US-08-937-993-37
79	166.5	12.8	244	1	US-08-762-129-1
80	163.5	12.5	319	2	US-08-977-847-1
81	163.5	12.5	319	2	US-09-195-021-1
82	163.5	12.5	317	3	US-09-109-205-18
83	162.5	12.5	317	3	US-08-940-424-5
84	162.5	12.5	360	4	US-09-740-028A-2
85	162	12.4	255	4	US-09-036-967A-21
86	161.5	12.4	274	4	US-09-370-700-21
87	161.5	12.4	335	3	US-09-740-028A-4
88	161.5	12.4	335	3	US-09-002-298-7
89	159.5	12.2	316	4	US-08-729-594A-36
90	159.5	12.2	316	4	US-08-937-993-36
91	159.5	12.2	316	4	US-08-940-424-2
92	158.5	12.2	335	3	US-09-002-298-6
93	156.5	12.0	335	3	US-09-109-205-19
94	154.5	11.8	317	2	US-08-977-847-3
95	154.5	11.8	317	2	US-09-195-021-3
96	154.5	11.8	317	4	US-08-940-424-4
97	154	11.8	318	4	US-09-605-785-339
98	154	11.8	318	4	US-09-439-313-339
99	154	11.8	318	4	US-09-352-616A-339
100	152	11.7	327	1	US-08-375-962B-12

Page 15

[illegible]

PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 22.38; Score 290.5; DB 9; Length 270;
Best Local Similarity 31.78; Pred. No. 4.2e-18;
Matches 86; Conservative 42; Mismatches 106; Indels 37; Gaps 8;

QY 1 MAACRSVKGIVAVITGASGLGLATAEIYVGGASAVLIDLPSGSGEAAKKLGNVVF 60
DB 1 MATGTR-YAGKVVYVTTGGRGIGIYRATVNSGARVYICDKDESGRALEQEL-PRAVF 58
QY 61 APADYTSKDVQALALAKKFEGRVDVAVNCAGIAVASKTYNLLKGGTHTLEDFQRYLDV 120
DB 59 ILICVTEDEDDVKTIVSERIRRFGRLCDVYNNAGHHPP-----ORPETSAQGFRODLEL 113
QY 121 NLMGFENYRLVAGEMGNEDDQGGQGVIIINTASVAFGQVQAAVYSAKSGIYVMTL 180
DB 114 NLGTITRLKALAYLRKSO-----GNVINISLVAIGQAQAVYVAFKQVMTMX 166
QY 181 PIADLAPIGIRVWTIAPLGFETPLLSLPEKVCNFIASQVPP-----SRL 227
DB 167 ALADESPYGRVNCISGNIWTFLEWEE-----LAALMPDRATIREGMLAQPLGRM 218
QY 228 GDPAEY-AHLVQAIENFPLNG-EVIRLDGA 256
DB 219 GQPAEYGAAYFLASEANFCIGIELLYTGGA 249

RESULT 25
US-09-978-192A-468
Sequence 468, Application US/09978192A
Patent No. US2002017553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertslen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630PIC9
CURRENT APPLICATION NUMBER: US/09/978,192A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/063311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/063364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334

1	CURRENT FILING DATE: 2001-10-15
2	PRIOR APPLICATION NUMBER: 09/918585
3	PRIOR FILING DATE: 2001-07-30
4	PRIOR APPLICATION NUMBER: 60/062250
5	PRIOR FILING DATE: 1997-10-17
6	PRIOR APPLICATION NUMBER: 60/064249
7	PRIOR FILING DATE: 1997-11-03
8	PRIOR APPLICATION NUMBER: 60/065311
9	PRIOR FILING DATE: 1997-11-13
10	PRIOR APPLICATION NUMBER: 60/066364
11	PRIOR FILING DATE: 1997-11-21
12	PRIOR APPLICATION NUMBER: 60/077450
13	PRIOR FILING DATE: 1998-03-10
14	PRIOR APPLICATION NUMBER: 60/077632
15	PRIOR FILING DATE: 1998-03-11
16	PRIOR APPLICATION NUMBER: 60/077641
17	PRIOR FILING DATE: 1998-03-11
18	PRIOR APPLICATION NUMBER: 60/077649
19	PRIOR FILING DATE: 1998-03-11
20	PRIOR APPLICATION NUMBER: 60/077791
21	PRIOR FILING DATE: 1998-03-12
22	PRIOR APPLICATION NUMBER: 60/078004
23	PRIOR FILING DATE: 1998-03-13
24	PRIOR APPLICATION NUMBER: 60/078686
25	PRIOR FILING DATE: 1998-03-20
26	PRIOR APPLICATION NUMBER: 60/078936
27	PRIOR FILING DATE: 1998-03-20
28	PRIOR APPLICATION NUMBER: 60/078910
29	PRIOR FILING DATE: 1998-03-20
30	PRIOR APPLICATION NUMBER: 60/078939
31	PRIOR FILING DATE: 1998-03-20
32	PRIOR APPLICATION NUMBER: 60/079294
33	PRIOR FILING DATE: 1998-03-25
34	PRIOR APPLICATION NUMBER: 60/079656
35	PRIOR FILING DATE: 1998-03-26
36	PRIOR APPLICATION NUMBER: 60/079664
37	PRIOR FILING DATE: 1998-03-27
38	PRIOR APPLICATION NUMBER: 60/079689
39	PRIOR FILING DATE: 1998-03-27
40	PRIOR APPLICATION NUMBER: 60/079663
41	PRIOR FILING DATE: 1998-03-27
42	PRIOR APPLICATION NUMBER: 60/079728
43	PRIOR FILING DATE: 1998-03-27
44	PRIOR APPLICATION NUMBER: 60/079786
45	PRIOR FILING DATE: 1998-03-27
46	PRIOR APPLICATION NUMBER: 60/079920
47	PRIOR FILING DATE: 1998-03-30
48	PRIOR APPLICATION NUMBER: 60/079923
49	PRIOR FILING DATE: 1998-03-30
50	PRIOR APPLICATION NUMBER: 60/080105
51	PRIOR FILING DATE: 1998-03-31
52	PRIOR APPLICATION NUMBER: 60/080107
53	PRIOR FILING DATE: 1998-03-31
54	PRIOR APPLICATION NUMBER: 60/080165
55	PRIOR FILING DATE: 1998-03-31
56	PRIOR APPLICATION NUMBER: 60/080194
57	PRIOR FILING DATE: 1998-03-31
58	PRIOR APPLICATION NUMBER: 60/080327
59	PRIOR FILING DATE: 1998-04-01
60	PRIOR APPLICATION NUMBER: 60/080328
61	PRIOR FILING DATE: 1998-04-01
62	PRIOR APPLICATION NUMBER: 60/080333
63	PRIOR FILING DATE: 1998-04-01
64	PRIOR APPLICATION NUMBER: 60/080334
65	PRIOR FILING DATE: 1998-04-01
66	PRIOR APPLICATION NUMBER: 60/081070
67	PRIOR FILING DATE: 1998-04-08
68	PRIOR APPLICATION NUMBER: 60/081449
69	PRIOR FILING DATE: 1998-04-08
70	PRIOR APPLICATION NUMBER: 60/081071
71	PRIOR FILING DATE: 1998-04-08
72	PRIOR APPLICATION NUMBER: 60/081195
73	PRIOR FILING DATE: 1998-04-08

PRIOR APPLICATION DATE:	NUMBER:	60/081203
PRIOR FILING DATE:	NUMBER:	1998-04-09
PRIOR APPLICATION NUMBER:	60/081229	
PRIOR FILING DATE:	NUMBER:	1998-04-09
PRIOR APPLICATION NUMBER:	60/081955	
PRIOR FILING DATE:	NUMBER:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081817	
PRIOR FILING DATE:	NUMBER:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081819	
PRIOR FILING DATE:	NUMBER:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081952	
PRIOR FILING DATE:	NUMBER:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081838	
PRIOR FILING DATE:	NUMBER:	1998-04-15
PRIOR APPLICATION NUMBER:	60/082568	
PRIOR FILING DATE:	NUMBER:	1998-04-21
PRIOR APPLICATION NUMBER:	60/082569	
PRIOR FILING DATE:	NUMBER:	1998-04-21
PRIOR APPLICATION NUMBER:	60/082704	
PRIOR FILING DATE:	NUMBER:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082804	
PRIOR FILING DATE:	NUMBER:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082700	
PRIOR FILING DATE:	NUMBER:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082797	
PRIOR FILING DATE:	NUMBER:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082796	
PRIOR FILING DATE:	NUMBER:	1998-04-23
PRIOR APPLICATION NUMBER:	60/083336	
PRIOR FILING DATE:	NUMBER:	1998-04-27
PRIOR APPLICATION NUMBER:	60/083322	
PRIOR FILING DATE:	NUMBER:	1998-04-28
PRIOR APPLICATION NUMBER:	60/083392	
PRIOR FILING DATE:	NUMBER:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083495	
PRIOR FILING DATE:	NUMBER:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083496	
PRIOR FILING DATE:	NUMBER:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083499	
PRIOR FILING DATE:	NUMBER:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083545	
PRIOR FILING DATE:	NUMBER:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083559	
PRIOR FILING DATE:	NUMBER:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083554	
PRIOR FILING DATE:	NUMBER:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083588	
PRIOR FILING DATE:	NUMBER:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083559	
PRIOR FILING DATE:	NUMBER:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083500	
PRIOR FILING DATE:	NUMBER:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083742	
PRIOR FILING DATE:	NUMBER:	1998-04-30
PRIOR APPLICATION NUMBER:	60/084366	
PRIOR FILING DATE:	NUMBER:	1998-05-05
PRIOR APPLICATION NUMBER:	60/084639	
PRIOR FILING DATE:	NUMBER:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084640	
PRIOR FILING DATE:	NUMBER:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084589	
PRIOR FILING DATE:	NUMBER:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084600	
PRIOR FILING DATE:	NUMBER:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084627	
PRIOR FILING DATE:	NUMBER:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084643	
PRIOR FILING DATE:	NUMBER:	1998-05-07
PRIOR APPLICATION NUMBER:	60/085339	

PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 22.3% Score 290.5; DB 9; Length 270;
Best Local Similarity 31.7%; Pred. No. 4, 2e-18;
Matches 86; Conservative 42; Mismatches 106; Indels 37; Gaps 8;

QY 1 MAAARSVKGLVAVITGASGLATPAERLVGGASAVLLDLPNSGGEQAOKLGNVVF 60
DB 1 MATGR-YAGKVVVYVGGGRGIGATVRAVNSGARVVICDXDESGRALEQL-PGAVF 58
QY 61 APADVTSEKDVQATLAKKFGRVAVVACAGIAVASKYNNLKKQTHLEDFORLAV 120
DB 59 ILCDVTDEDVKTIVSETIRFGRDGVNNASHRRP-----QREETSAGCFRLLEL 113
QY 121 NLMTFNVIRLVAGEMQNEPDGQGVLIINTASVAEAGVGAAYASAKGIVGML 180
DB 114 NLGTVTLFLALPYLRKSQ-----GNVINISLVGAIGQAVPYATKAVTAMRK 166
QY 181 PIADLAPIGRWTIRPGFGLTSLSEKYNLASGVRP-----STL 227
DB 167 ALADESPYGVAVNCISPGNIMPLMBE-----LAALPDPRAITREGMIAQLGR 218
QY 228 GDPAEV-AHLVQATLLENPLNG-EVIRLDGA 256
DB 219 GPFAVGAAVFLASEANFCTGIELVLTGSA 249

RESULT 24
US-09-978-697-468
Sequence 468, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowskl, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillap, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978, 697

ORGANISM: Gluconobacter oxydans
US-09-802-853-6

Query Match 22.4% Score 292.5; DB 10; Length 262;
Best Local Similarity 31.6% Pred. No. 2.7e-18;
Matches 86; Conservative 41; Mismatches 110; Indels 35; Gaps 7;

QY 6 RSVKGLVAVITGASGLGLATATRLVGGASAVLIDPNSG---GEAQAARKLGNVYFAP 62
DB 3 KRFNKKVCLVYGAGNIGLALALRLAEERGTALALDDNMRLEAEASVREKGYEASVY 62
QY 63 ADVTSKDVOTALALAKKRFGRVDVAVNAGIAVASKYNNKKGQTHLEDFQVLDVNL 122
DB 63 CVTSEEAIVIGTVDSVDFGKIDFLFNAGYOGA----FAPVQDYFSDDFARVLTINV 117
QY 123 MGEFVIRLVAGEM-GONEPDGGGGRGYITINVASVAFAEGOVGOAAVSASKGIVGMLP 181
DB 118 TGAFLVLAQVSKQMTQN-----YGRIVNTASAGVKGPPNMAAYGASGAILTLET 170
QY 182 IARDLAPIGIRVMTIAPGLF-----GTPPLTSLPEKYCNFLASQVPPPS 225
DB 171 AALDLAPYIRVNAISPGMGPFMRQVELQAVGQYFSTDPKVVAAQMGISVPM-R 229
QY 226 RLGDPAEVAHLVQAIT--ENPFLNGEVIRLDG 225
DB 230 RYGDINEIRGVVAFLIGDDSSFTWGVNLPING 261

RESULT 23
US-09-978-295A-468
Sequence 468, Application US/09978295A
Patent No. US2002015606A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819

Thu Jun 26 06:55:09 2003

us-09-931-186-6.rapb

Page 10

TYPE: PRT
ORGANISM: Bacillus megaterium
US-09-479-040-9

Query Match 23.1%; Score 301; DB 9; Length 247;
Best Local Similarity 29.1%; Pred. No. 4.4e-19;
Matches 78; Conservative 59; Mismatches 93; Indels 38; Gaps 9;

7 SVKGLVAVITGASGLATAEERLVGQ-----ASAVLLDLPNSGGEAQAOK 53
3 TLQKVAIVTGSAGIAITRELSNGVAVAVNYSKESABAIYKEIKDNGEA---- 58
54 LGNNVAPADYSEKIDVQALALAKKFRGVAVVACAIYVASKTYNKK-GCHTLE 112
59 ----IAVQADVSVDOAKHLIEETKAFQDLVNNAGI---TRDRSKKLGE----E 106
113 DFOHVDVNLMTFNVIRLVAGENGQNEPDGQGVYINTASVAEFGVQQAAYSASK 172
107 DMKVIDVNLHSVNTSALTLHLESE---GGR---VINISSIGAGGQNTYSAK 160
173 GGIYGMILPFIARDLAPIGIRMTIAPGLFGTPLLFSPEKVCNFLASQVFPBRIDPAE 232
161 AGMLGFTKSLALELAKGVYVNAICPGFIETEMVAIPEDVRAKIVAKIP-TRLLGHAEE 219
233 YAH-LVQAIIENPFLNGEVIRLDGAIRM 259
220 IARGVYIAKDGAVIITGQOLNINNGLYM 247

RESULT 20
US-09-773-748-1
Sequence 1, Application US/09773748
Publication No. US20020187537A1
GENERAL INFORMATION:
APPLICANT: Wada, Masaru
TITLE OF INVENTION: Levodione reductase gene and use thereof
FILE REFERENCE: Levodione reductase
CURRENT APPLICATION NUMBER: US/09/773,748
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: EP00101665-8
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 1
LENGTH: 267
TYPE: PRT
ORGANISM: Corynebacterium aquaticum
US-09-773-748-1

Query Match 22.8%; Score 297.5; DB 9; Length 267;
Best Local Similarity 31.8%; Pred. No. 9.9e-19;
Matches 84; Conservative 46; Mismatches 97; Indels 37; Gaps 9;

12 VAVITGASGLATAEERLVGQASAVLLDLPNSGGEAQAOKL-----GNNVYAPADYT 66
15 VVLIIGSGSGGRATAVRAVLAAGAKLSIVDVSSEGLASKAIVLEIAPDAVLELVADVS 74
67 SKDVQVIALAKKFGFRVDVAVNAGIYAVASKITNKKQTHLEDPQVILDVNLMTF 126
75 DDAQVAVYVATTEFRGRIDGFFNNAGLEBKO-----NPTEFTAEEDKVAISILRGVF 129
127 ----VIRLVAGENGQNEPDGQGVYINTASVAEFGVQQAAYSASKGIGVMTLPI 182
130 LGLVNLKIMR-----EGGS--GMVYNTASVGIGINGISGYAAAKHGVVGLTRNS 179
183 AADLAPIGIRMTIAPGLFGTPLLFSPEKVCNFLASQVFPBRIDPAEY 233
180 AVEYGRYGRIRINAIAGAITPMEVNSMKOLDPENPRKAAEEFI--QVNPSSKRYEAPDI 237
234 AHIYQAIIN--PFLNGEVIRLDG 255
238 AAVVAFLLSDASVYNAVIVPIDG 261

RESULT 21
US-10-307-385-6
Sequence 6, Application US/10307385
Publication No. US2003007797A1
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, MASAKAZU
APPLICANT: TONOUCHI, NAOTO
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: YOKOZAKI, KENZO
TITLE OF INVENTION: XYLTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
FILE REFERENCE: 0010-1024-0
CURRENT APPLICATION NUMBER: US/10/307,385
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US/09/363,189
PRIOR FILING DATE: 1998-07-26
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 262
TYPE: PRT
ORGANISM: Gluconobacter oxydans
US-10-307-385-6

6 RSVKGLVAVITGASGLATAEERLVGQASAVLLDLPNSG---GEAQAOKLGNVYAP 62
3 KKEGKVCVLTGAGNIGATATLAEESTALALDMNEALEKAVSYREKVEARSTV 62
63 ADYSEKDVQVIALAKKFGFRVDVAVNAGIYAVASKITNKKQTHLEDPQVILDVNL 122
63 CDVTSSEAVIGTDSVVRDEGKIDFLFNAGVGA-----FAPVODYPSDDFARVLTIV 117
123 MGFNVIRLVAGEM-GQNEPDGQGVYINTASVAEFGVQQAAYSASKGIGVMTLP 181
118 TGAHFVYIAKASROMIION-----YGRIVNTASMGVGRPPMAAYGASKGAILTLET 170
182 IARDLAPIGIRMTIAPGLF-----GTPLLSLPEKVCNFLASQVFPBRID 225
171 AADLAPYINIRVNAISPGLVGPFFMWERQVELQAKYGSQYFSFDPVAVQOMIGVPM-R 229
226 RLGDPAEYAHVQAII--ENPFLNGEVIRLDG 255
230 RYGDINEIPGVAVFLLGDSSFMTGVNLPIDG 261

Query Match 22.4%; Score 292.5; DB 9; Length 262;
Best Local Similarity 31.6%; Pred. No. 2.7e-18;
Matches 86; Conservative 41; Mismatches 110; Indels 35; Gaps 7;

US-09-802-853-6
Sequence 6, Application US/09802853
Patent No. US20010034049A1
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, MASAKAZU
APPLICANT: TONOUCHI, NAOTO
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: YOKOZAKI, KENZO
TITLE OF INVENTION: XYLTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
FILE REFERENCE: 0010-1024-0
CURRENT APPLICATION NUMBER: US/09/802,853
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 09/363,189
PRIOR FILING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: JP10-216047
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 262
TYPE: PRT

OY 247 NGEYIRLDGATRM 259
 Db 223 TGHVLYVDGGLQL 235

RESULT 17

US-09-815-242-10921
 ; Sequence 10921, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlssen, Karl L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; TITLE OF INVENTION: Prokaryotes
 ; FILE REFERENCE: EUTRA.011a
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 10921
 ; LENGTH: 245
 ; TYPE: PRF
 ; ORGANISM: Enterococcus faecalis
 US-09-815-242-10921

Query Match 23.7%; Score 308.5; DB 10; Length 245;
 Best Local Similarity 33.3%; Pred. No. 9.3e-20;
 Matches 83; Conservative 38; Mismatches 109; Indels 19; Gaps 5;

OY 15 ITGASGSLGATAEHLVGGASAVYLD---LPNSGGEAOKKIGNNVFAPADVTSEKD 70
 Db 10 ITGSTRGIGKAVALLAFAGEAHYVINGSEITPEKROIEA--FGVKCIGISGDISPDA 67
 OY 71 VOTALAKGRFGRVAVANCAGIYVASKTYNLKKGOTHTLEDFORVLDVNMGTENVIR 130
 Db 68 AGEMIOATVDDGSDILVNNAGIT-----NDKLLMTKEDFNACDINLVGFNNQ 121
 OY 131 LVAGMGONEPDGGRGVYIINTASVAFEGOVGOAASASAKGIVGMLPIARDLIAIG 190
 Db 122 QAVKEMMQ-----RSGRITMASVSGLMGVGANYAASAGVGTKSVAREVAPRG 175
 OY 191 IRVMTIAPGLFTPLLTSLPEKVCNFLASQVFPFSLRDPPEYAHLVQAIIEPFLNGEV 250
 Db 176 ITCNALAPGFIQTEMTDVLSERVKTKOMNAQIPLGT--FGVBDVATAIFLAKSPYITGOV 234
 OY 251 IRLDGAIRM 259
 Db 235 VAVDGLVAV 243

RESULT 18
 US-09-931-186-15
 ; Sequence 15, Application US/09931186

Patent No. US20020132319A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ABREO, MELWYN A.
 ; APPLICANT: AGRE, CHARLES S.
 ; APPLICANT: AUST, ROBERT
 ; APPLICANT: KISSINGER, CHARLES R.
 ; APPLICANT: MARGOSIAK, STEVE
 ; APPLICANT: MENG, JERRY J.
 ; APPLICANT: PELLETIER, LAURA A.
 ; APPLICANT: REUTO, PAUL A.
 ; APPLICANT: SHOMALTER, RICHARD E.
 ; APPLICANT: TEMPCZYK-RUSSELL, ANNA
 ; APPLICANT: THOMSON, JIM
 ; APPLICANT: VANDERPOOL, DARIN
 ; APPLICANT: VILLAFRANCA, J. ERNEST
 ; TITLE OF INVENTION: PEPTIDE MOTIF OF HUMAN ERAB/RAD2, ITS X-RAY CRYSTAL
 ; TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
 ; FILE REFERENCE: 0125-0049
 ; CURRENT APPLICATION NUMBER: US/09/931,186
 ; CURRENT FILING DATE: 2001-08-17
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 15
 ; LENGTH: 253
 ; TYPE: PRF
 ; ORGANISM: Streptomyces hydrogenans
 US-09-931-186-15

Query Match 23.4%; Score 305.5; DB 10; Length 253;
 Best Local Similarity 33.3%; Pred. No. 1.8e-19;
 Matches 84; Conservative 48; Mismatches 101; Indels 19; Gaps 7;

OY 8 VKGLVAVITFGASGLGATAEHLVGGASAVYLDLPNSGGEAOKKIGNNVFAPADVT 67
 Db 3 LSKRTYIITGSGALGAEARQAVAGARVADVDEGAATARELGDAARQHDVYI 62
 OY 68 EKDVQALALAKRFRVAVANCAGIYVASKTYNLKKGOTHTLEDFORVLDVNMGTEN 127
 Db 63 EEDMQRVAVAREFSSVDDLVNNAISTGMFL-----ETESVERFRVVEINLVGVI 116
 OY 128 VIRLVAGMGONEPDGGRGVYIINTASVAFEGOVGOAASASAKGIVGMLPIARDLIA 187
 Db 117 GMRVTPAM---KDAAG--GSIVNLSAAGMLGLTSSYKSKGVGSLKLAIVEIG 170
 OY 188 PIGIRVMTIAPGLFTPLLTSLPEKVCNFLASQVFPFSLRDPPEYAHLVQAIIE--N 243
 Db 171 TDIRVNSVHRGMYTPTMETGTIRGEGNY--PNTPM--GRVGPGLIAGAVVKKLLSDTS 227
 OY 244 PFLNGEYIRLDG 255
 Db 228 SYVGAELAVDG 239

RESULT 19
 US-09-479-040-9
 ; Sequence 9, Application US/09479040
 ; Publication No. US20020182690A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MCCOOL, Gabriel J.
 ; APPLICANT: Cannon, Maura C.
 ; APPLICANT: Cannon, Francis C.
 ; APPLICANT: Valentin, Henry E.
 ; APPLICANT: Gruys, Kenneth J.
 ; TITLE OF INVENTION: POLYHYDROXYALKANATE BIOSYNTHESIS ASSOCIATED PROTEINS
 ; TITLE OF INVENTION: AND CODING REGION IN BACILLUS MEGATERIUM
 ; FILE REFERENCE: M0B1212
 ; CURRENT APPLICATION NUMBER: US/09/479,040
 ; CURRENT FILING DATE: 2000-01-07
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 9
 ; LENGTH: 247


```

; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: ABREO, MELVYN A.
; APPLICANT: AGRE, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISTINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOWALTER, RICHARD E.
; APPLICANT: TEMCZYK-RUSSELL, ANNA
; APPLICANT: THOMSON, JIM
; APPLICANT: VANDERPOOL, DARIN
; APPLICANT: VILLAFRANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
; TITLE OF INVENTION: OF INHIBITORS THEREOF
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931,186
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 259
; TYPE: PRP
; ORGANISM: Homo sapiens
; US-09-931-186-17

Query Match      25.5%; Score 332.5; DB 10; Length 259;
Best Local Similarity 31.2%; Pred. No. 7,4e-22;
Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;

QY      8 VAGLVAVITGGASGIGLTAERLVQGASAVLDDLPNSGGEQAOKL-----GN 56
      :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      7 LKSALALVYGAGSGIGRAVSVRLAGEGATVAAACDDRAAAGETVLLGGPGSKGPPRGN 66
      :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY      57 NVYFAPADVTSEKDVQJALALAKKFRGR-VDVAVNCAGIAVASKTYNKKGTHTLEDFO 115
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      67 HNAF-QADVSEARARCOLLEQVQACFSRPSVYVSCAGITODEFLHSE-----DDWD 119
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY      116 RYLDVNLKGTENVYVILVAGMGONBPDGCGRGVYIINTASVAFEGVGAASAKSGIGI 175
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      120 KYIAVNLKGTFLYTAAGALVSN-----GCRGSIINISSIVKGKGVNGQTVYASKKGV 174
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY      176 VGMTPLIARDLAPIGIRVYTIAPGLFGLTSLPEKVCNPLASQVPPSRLDPAEYAH 235
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      175 IGLTQTAARELGRHGRCHNSVLPGLATFPMQKVQKVDKITEMIPM-GHLDPEDEVAD 233
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY      236 LVQ--AIENPFLNGEVIRLDGAIKM 259
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      234 VVAFLESDSGYITGTSTVEVTGLPM 259
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 13
US-09-815-242-13360
; Sequence 13360, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078

```

```

; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13360
; LENGTH: 243
; TYPE: PRP
; ORGANISM: Streptococcus pneumoniae
; US-09-815-242-13360

Query Match      25.4%; Score 331.5; DB 10; Length 243;
Best Local Similarity 35.5%; Pred. No. 8,4e-22;
Matches 89; Conservative 36; Mismatches 103; Indels 23; Gaps 6;

QY      15 ITGASGLGATARLVQGASAVLDDLPNSGE-----AQAKKIGNVYFAPADVTSE 68
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      10 ITGSSRGIGLAIARKEAQAQANVY-----NSRGAISELLAEFSNGIKVYPSGSDVF 65
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY      69 KDVTALALAKKGRGVAVVNCAGIAVASKTYNKKGTHTLEDFOYLDVNLKGTENV 128
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      66 ADARIMDQIAELGSDVLYNNNGI--TQDTLTKM---TEADFEKVKVNLTGAFNM 119
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY      129 IRVAVMGONBPDGCGRGVYIINTASVAFEGVGAASAKSGIGVGTTLIARDLAP 188
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      120 TQSVL-----KPMKRAEGAIIMSSVVGIMGNGIGANTPAASAGLIGFTKSAKEVAS 173
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY      189 IGIRVMTIAPGLFGLTSLPEKVCNPLASQVPPSRLDPAEYAHVQAIENPFLNG 248
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      174 RNIVNVNAPBMISDWTALISDKIKENTLAQIPM-KEFGAGQEVADLVYFLAGQDVLTG 232
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY      249 EVIRLDGAIKM 259
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB      233 QVIAIDGGLSM 243
      :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 14
US-09-815-242-13581
; Sequence 13581, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625

```

```

; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-966-245

Query Match
Best Local Similarity 99.6%; Pred. No. 3.2e-93;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

87.1%; Score 1136; DB 9; Length 227;
Best Local Similarity 99.6%; Pred. No. 3.2e-93;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 35 ASAVLLDLPNSGGGAQAKLGNVVFAPADVTSEKDVQALALAKKRGVDVAVNCAGI 94
DB 1 ASAVLLDLPNSGGGAQAKLGNVVFAPADVTSEKDVQALALAKKRGVDVAVNCAGI 60
QY 95 AVASKTYNLKKGQHTLDEDFQRYLDVNLMTGFNVIRLVAGEMGONEPDGGRGVYIINTA 154
DB 61 AVASKTYNLKKGQHTLDEDFQRYLDVNLMTGFNVIRLVAGEMGONEPDGGRGVYIINTA 120
QY 155 SVAAFEGVGQAAYASASKSGIVGNTLPYARDLAPIGIRVMTIAPGLFSTPLTSLPERVC 214
DB 121 SVAAFEGVGQAAYASASKSGIVGNTLPYARDLAPIGIRVMTIAPGLFSTPLTSLPERVC 180
QY 215 NFLASQVPPPSRLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKMQP 261
DB 181 NFLASQVPPPSRLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKMQP 227

RESULT 10
US-10-143-090-245
; Sequence 245, Application US/10143090
; Publication No. US20030069406a1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
```

```

; ORGANISM: Homo sapiens
US-10-143-090-245

Query Match
Best Local Similarity 87.1%; Score 1136; DB 9; Length 227;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 35 ASAVLLDLPNSGGGAQAKLGNVVFAPADVTSEKDVQALALAKKRGVDVAVNCAGI 94
DB 1 ASAVLLDLPNSGGGAQAKLGNVVFAPADVTSEKDVQALALAKKRGVDVAVNCAGI 60
QY 95 AVASKTYNLKKGQHTLDEDFQRYLDVNLMTGFNVIRLVAGEMGONEPDGGRGVYIINTA 154
DB 61 AVASKTYNLKKGQHTLDEDFQRYLDVNLMTGFNVIRLVAGEMGONEPDGGRGVYIINTA 120
QY 155 SVAAFEGVGQAAYASASKSGIVGNTLPYARDLAPIGIRVMTIAPGLFSTPLTSLPERVC 214
DB 121 SVAAFEGVGQAAYASASKSGIVGNTLPYARDLAPIGIRVMTIAPGLFSTPLTSLPERVC 180
QY 215 NFLASQVPPPSRLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKMQP 261
DB 181 NFLASQVPPPSRLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKMQP 227

RESULT 11
US-09-920-923-41
; Sequence 41, Application US/09920923
; Publication No. US2003002273A1
; GENERAL INFORMATION:
; APPLICANT: Tsigankov, Yuri
; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
; FILE REFERENCE: Improved Fermentative Carotenoid
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US/09/920,923
; PRIOR FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Flavobacterium sp. R1534
US-09-920-923-41

Query Match
Best Local Similarity 51.0%; Score 664.5; DB 9; Length 388;
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VKGLVAVITIGASGLGATAEERLVGGASAVLLDLPNSGGGAQAKLGNVVFAPADVTS 67
DB 143 IEGRVFVVTGAASGLGASARMLAQGAKVYIADL-----ABPKAPPGAVHAACDVTD 196
QY 68 EKQVQTLAAKRFQGVNDVAVNCAGIYASAKTYNLKKGQHTLDEDFQRYLDVNLMTGFN 127
DB 197 ATAAQTAIALATRFQGLDGLVNCAGIAPAEERY--LGRQPRGLDSFAVAIVTILGSEN 254
QY 128 VIRLVAGEMGONEPDGGRGVYIINTASVAAFEGVGQAAYASASKSGIVGNTLPYARDIA 187
DB 255 MARLAEAAMARNEPVR-GERGVIVNTASIAACQGOIGOVAYYASAKGAVGNTLPMARDIA 313
QY 188 PIGIRVMTIAPGLFSTPLTSLPERVCNPLASQVPPPSRLGDPAEYAHVQAIIENPFLN 247
DB 314 RHGIRVMTIAPGLFSTPLTSLPERVGLDPOVDVDSLGAAVPPPSRLGEPSEYAAALHIIAMPMLN 373
QY 248 GEVIRLDGAIKMQP 261
DB 374 GEVIRLDGAIKMQP 387

RESULT 12
US-09-931-186-17
; Sequence 17, Application US/09931186
```


Thu Jun 26 06:55:09 2003

us-09-931-186-6.rapb

Page 5

Best Local Similarity 99.68; Pred. No. 3.2e-93;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	35	ASAVLLEDPSSGGEAAKKTGNNVFPADPVTSEKDVOGTALALAGKGRDVAWNCAGI	94
Db	1	ASAVLLEDPSSGGEAAKKTGNNCVPADPVTSEKDVOGTALALAGKGRDVAWNCAGI	60
QY	95	AVASKTYNLKKGQTHLEDFQRLVDVNLGTFENVIRLVAEGEKGNEPDQGGQRCGIINTA	15
Db	61	AVASKTYNLKKGQTHLEDFQRLVDVNLGTFENVIRLVAEGEKGNEPDQGGQRCGIINTA	120
QY	155	SVAAFEQVQQAAYSASKGIVGMLPIARDLAPIGIRMTIARPLSEGTPLITSIPXYC	21
Db	121	SVAAFEQVQQAAYSASKGIVGMLPIARDLAPIGIRMTIARPLSEGTPLITSIPXYC	180
QY	215	NFLASQVFPFSRLGDPAEVAHLVQALITENPFLNGEYIRLDGAIIRQOP	261
Db	181	NFLASQVFPFSRLGDPAEVAHLVQALITENPFLNGEYIRLDGAIIRQOP	227

RESULT 8
US-09-966-262-245

```

; Sequence 245, Application US/09966262
; Publication No. US20030050461A1
; GENERAL INFORMATION:

```

APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
CURRENT APPLICATION NUMBER: US/09/966,262
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: US 09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/05311
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: US 60/041,277
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/042,344
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,276
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,281
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/048,094
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,350
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,188
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,135
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/050,937
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,187
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,099
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,352
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,186
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,069
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,095
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,131
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,096
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,355
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,160
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,351

```

? PRIOR FILING DATE: 1997-05-30
? PRIOR APPLICATION NUMBER: US 60/048,154
? PRIOR FILING DATE: 1997-05-30
? PRIOR APPLICATION NUMBER: US 60/054,804
? PRIOR FILING DATE: 1997-08-05
? PRIOR APPLICATION NUMBER: US 60/056,370
? PRIOR FILING DATE: 1997-08-19
? PRIOR APPLICATION NUMBER: US 60/060,863
? PRIOR FILING DATE: 1997-10-02
? NUMBER OF SEQ ID NOS: 343
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 245
?
? LENGTH: 227
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-966-262-245

```

Query Match	87.1%	Score 1136;	DB 9;	Length 227;
Best Local Similarity	99.6%	Pred. No. 3.2e-93;		
Matches 226; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	35	ASAVLLDLPDSGGGAQAKLIGNNVAFAPADYTSKDQVDTALALAKGFRGVADVANAGI	94
Db	1	ASAVLLDLPDSGGGAQAKLIGNNVAFAPADYTSKDQVDTALALAKGFRGVADVANAGI	60
Qy	95	AVASKTYNKKGGTHTLDFQRYLDVNMKGTFNVIRLVAGEMGQNEPDGGQGVIIINTA	154
Db	61	AVASKTYNKKGGTHTLDFQRYLDVNMKGTFNVIRLVAGEMGQNEPDGGQGVIIINTA	120
Qy	155	SVAAEBOQGOAAYSASKSGGIYGMPLPARDLAPIGIRVMTIAPGLSTPLITSLPKYC	214
Db	121	SVAAEBOQGOAAYSASKSGGIYGMPLPARDLAPIGIRVMTIAPGLSTPLITSLPKYC	180
Qy	215	NFLASQVPPPSRLGDPAEYAHVQALITENPFLNGVIRLDGAIKRP	261
Db	181	NFLASQVPPPSRLGDPAEYAHVQALITENPFLNGVIRLDGAIKRP	227

RESULT 9
US-09-983-966-245

```

; Sequence 245, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:

```

```

1  APPLICANT: young et al.
2  TITLE OF INVENTION: 87 Human Secreted Proteins
3  FILE REFERENCE: P2004P1
4  CURRENT APPLICATION NUMBER: US/09/983,966
5  CURRENT FILING DATE: 2001-10-29
6  PRIOR APPLICATION NUMBER: 09/154,707
7  PRIOR FILING DATE: 1998-09-17
8  PRIOR APPLICATION NUMBER: PCT/US98/05311
9  PRIOR FILING DATE: 1998-03-19
10 PRIOR APPLICATION NUMBER: US 60/044,277
11 PRIOR FILING DATE: 1997-03-21
12 PRIOR APPLICATION NUMBER: US 60/042,344
13 PRIOR FILING DATE: 1997-03-21
14 PRIOR APPLICATION NUMBER: US 60/041,276
15 PRIOR FILING DATE: 1997-03-21
16 PRIOR APPLICATION NUMBER: US 60/041,281
17 PRIOR FILING DATE: 1997-03-21
18 PRIOR APPLICATION NUMBER: US 60/048,094
19 PRIOR FILING DATE: 1997-05-30
20 PRIOR APPLICATION NUMBER: US 60/048,350
21 PRIOR FILING DATE: 1997-05-30
22 PRIOR APPLICATION NUMBER: US 60/048,188
23 PRIOR FILING DATE: 1997-05-30
24 PRIOR APPLICATION NUMBER: US 60/048,135
25 PRIOR FILING DATE: 1997-05-30
26 PRIOR APPLICATION NUMBER: US 60/050,937
27 PRIOR FILING DATE: 1997-05-30
28 PRIOR APPLICATION NUMBER: US 60/048,187
29 PRIOR FILING DATE: 1997-05-30
30 PRIOR APPLICATION NUMBER: US 60/048,099

```

Thu Jun 26 06:55:09 2003

us-09-931-186-6.rapb

```
Db 61 AAPADVTSEKVOFTALALAKKRGVAVYAVACAGIAVASKTYNKKQOTHTLEDFOKVLV 120
QY 121 NLMGTFENVIRLVAGEMQNEPDGQGVLIINTASVAAREGVGAQAAVSASKSGIVGML 180
Db 121 NLMGTFENVIRLVAGEMQNEPDGQGVLIINTASVAAREGVGAQAAVSASKSGIVGML 180
QY 181 PIARDLAPIGIRVMTIPGIFGFPPLLSLEPEKCNLASVPPPSLGDPAEYAHVQAI 240
Db 181 PIARDLAPIGIRVMTIPGIFGFPPLLSLEPEKCNLASVPPPSLGDPAEYAHVQAI 240
QY 241 IENPFLNGEVIIRLDGAIKMQP 261
Db 241 IENPFLNGEVIIRLDGAIKMQP 261

RESULT 6
US-09-931-186-2
; Sequence 2, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: AGREO, MELWYN A.
; APPLICANT: AGREST, ROBERT
; APPLICANT: AUSTR, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REISTO, PAUL A.
; APPLICANT: SHOWALTER, RICHARD E.
; APPLICANT: TEMPCZYK-RUSSELL, ANNA
; APPLICANT: THOMSON, JIM
; APPLICANT: VANDERPOOL, DARIN
; APPLICANT: VILLAFRANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
; TITLE OF INVENTION: OF INHIBITORS THEREOF
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931,186
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: full length mutant ERAB C214R
US-09-931-186-2

Query Match 98.7%; Score 1287; DB 10; Length 261;
Best Local Similarity 99.2%; Pred. No. 1.5e+106;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
RESULT 7
US-09-984-245-245
; Sequence 245, Application US/09984245
; Patent No. US20020165374A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P
; CURRENT APPLICATION NUMBER: US/09/984,245
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-245-245

Query Match 87.1%; Score 1136; DB 9; Length 227;
```

```
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
TITLE OF INVENTION: OF INHIBITORS THEREOF
FILE REFERENCE: 0125-0049
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 20
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214A
US-09-931-186-20
```

```
Query Match          98.8%; Score 1289; DB 10; Length 261;
Best Local Similarity 99.2%; Pred. No. 8.2e-107;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 MAAACRSYKGLAVITGGASGLGATAEERLVGQASAVLLDLPNSGGEQAQAKKLGNNVF 60
DB 1 MAAACRSYKGLAVITGGASGLGATAEERLVGQASAVLLDLPNSGGEQAQAKKLGNNVF 60
QY 61 APADVSEKDVOTATLAKGKFGVDVAVNCAGIAVASKTYNLKKGOTHTLEDFORVLDV 120
DB 61 APADVSEKDVOTATLAKGKFGVDVAVNCAGIAVASKTYNLKKGOTHTLEDFORVLDV 120
QY 121 NMGTFFVIRLVAGEMGQNEPDGQGGVGIINTASVAAFEGVQQAAYSASKSGIYGMTL 180
DB 121 NMGTFFVIRLVAGEMGQNEPDGQGGVGIINTASVAAFEGVQQAAYSASKSGIYGMTL 180
QY 181 PIADLAPIGIRVMTIAPGLFGTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHVQAI 240
DB 181 PIADLAPIGIRVMTIAPGLFGTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHVQAI 240
QY 241 IENPFLNGEYIRLDGAIKMQP 261
DB 241 IENPFLNGEYIRLDGAIKMQP 261
```

```
RESULT 4
US-09-931-186-4
Sequence 4, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGRE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
TITLE OF INVENTION: OF INHIBITORS THEREOF
FILE REFERENCE: 0125-0049
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 4
LENGTH: 261
TYPE: PRT
```

```
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C5V
US-09-931-186-4
```

```
Query Match          98.8%; Score 1289; DB 10; Length 261;
Best Local Similarity 99.2%; Pred. No. 1e-106;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 MAAACRSYKGLAVITGGASGLGATAEERLVGQASAVLLDLPNSGGEQAQAKKLGNNVF 60
DB 1 MAAACRSYKGLAVITGGASGLGATAEERLVGQASAVLLDLPNSGGEQAQAKKLGNNVF 60
QY 61 APADVSEKDVOTATLAKGKFGVDVAVNCAGIAVASKTYNLKKGOTHTLEDFORVLDV 120
DB 61 APADVSEKDVOTATLAKGKFGVDVAVNCAGIAVASKTYNLKKGOTHTLEDFORVLDV 120
QY 121 NMGTFFVIRLVAGEMGQNEPDGQGGVGIINTASVAAFEGVQQAAYSASKSGIYGMTL 180
DB 121 NMGTFFVIRLVAGEMGQNEPDGQGGVGIINTASVAAFEGVQQAAYSASKSGIYGMTL 180
QY 181 PIADLAPIGIRVMTIAPGLFGTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHVQAI 240
DB 181 PIADLAPIGIRVMTIAPGLFGTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHVQAI 240
QY 241 IENPFLNGEYIRLDGAIKMQP 261
DB 241 IENPFLNGEYIRLDGAIKMQP 261
```

```
RESULT 5
US-09-931-186-23
Sequence 23, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGRE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
TITLE OF INVENTION: OF INHIBITORS THEREOF
FILE REFERENCE: 0125-0049
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 23
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214S
US-09-931-186-23
```

```
Query Match          98.8%; Score 1289; DB 10; Length 261;
Best Local Similarity 99.2%; Pred. No. 1e-106;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 MAAACRSYKGLAVITGGASGLGATAEERLVGQASAVLLDLPNSGGEQAQAKKLGNNVF 60
DB 1 MAAACRSYKGLAVITGGASGLGATAEERLVGQASAVLLDLPNSGGEQAQAKKLGNNVF 60
QY 61 APADVSEKDVOTATLAKGKFGVDVAVNCAGIAVASKTYNLKKGOTHTLEDFORVLDV 120
```

93 233 17.9 311 9 US-09-738-626-3819 Sequence 3819, Ap
94 231 17.7 261 10 US-09-815-242-5813 Sequence 5813, Ap
95 225.5 17.3 247 10 US-09-815-242-11342 Sequence 11342, A
96 224 17.2 254 10 US-09-741-669-411 Sequence 411, App
97 223.5 17.1 900 9 US-10-060-230-15 Sequence 15, Appl
98 223.5 17.1 900 9 US-10-060-230-17 Sequence 17, Appl
99 222.5 17.1 247 10 US-09-815-242-11514 Sequence 11514, A
100 217.5 16.7 233 10 US-09-815-242-10279 Sequence 10279, A

ALIGNMENTS

RESULT 1

US-09-931-186-6
Sequence 6, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAR, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C58V
US-09-931-186-6

Query Match 100.0%; Score 1304; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 4.7e-108;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACRSVKGIVAVITGGASGLGATFAERLVGGASAVILDPNSGGEQAOKLGNVVF 60
DB 1 MAACRSVKGIVAVITGGASGLGATFAERLVGGASAVILDPNSGGEQAOKLGNVVF 60
QY 61 APADVTSKDVQVOTALAKGKFGVDVAVNCAGIYASRTYLNKKGQTHLEDFORVLDV 120
DB 61 APADVTSKDVQVOTALAKGKFGVDVAVNCAGIYASRTYLNKKGQTHLEDFORVLDV 120
QY 121 NLMGTFNVIRLVAGEKQNEPDGQGVIIINTASVAAEFGVGOAAYSASKGIYGMTL 180
DB 121 NLMGTFNVIRLVAGEKQNEPDGQGVIIINTASVAAEFGVGOAAYSASKGIYGMTL 180
QY 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKYCNFLASQVPPSRIGDPAEYAHVQAI 240
DB 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKYCNFLASQVPPSRIGDPAEYAHVQAI 240
QY 241 IENPFLNGEYIRLDGAIRMOP 261
DB 241 IENPFLNGEYIRLDGAIRMOP 261

RESULT 2

US-09-931-186-8
Sequence 8, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAR, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: wild type ERAB
US-09-931-186-8

Query Match 99.6%; Score 1299; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 1.3e-107;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAACRSVKGIVAVITGGASGLGATFAERLVGGASAVILDPNSGGEQAOKLGNVVF 60
DB 1 MAACRSVKGIVAVITGGASGLGATFAERLVGGASAVILDPNSGGEQAOKLGNVVF 60
QY 61 APADVTSKDVQVOTALAKGKFGVDVAVNCAGIYASRTYLNKKGQTHLEDFORVLDV 120
DB 61 APADVTSKDVQVOTALAKGKFGVDVAVNCAGIYASRTYLNKKGQTHLEDFORVLDV 120
QY 121 NLMGTFNVIRLVAGEKQNEPDGQGVIIINTASVAAEFGVGOAAYSASKGIYGMTL 180
DB 121 NLMGTFNVIRLVAGEKQNEPDGQGVIIINTASVAAEFGVGOAAYSASKGIYGMTL 180
QY 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKYCNFLASQVPPSRIGDPAEYAHVQAI 240
DB 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKYCNFLASQVPPSRIGDPAEYAHVQAI 240
QY 241 IENPFLNGEYIRLDGAIRMOP 261
DB 241 IENPFLNGEYIRLDGAIRMOP 261

RESULT 3

US-09-931-186-20
Sequence 20, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAR, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA

Thu Jun 26 06:55:09 2003

us-09-931-186-6.rapb

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 14:32:58 ; Search time 20.333 Seconds
(without alignments)
1388.950 Million cell updates/sec

Title: US-09-931-186-6.
Perfect score: 1304
Sequence: 1 MAACRSVKGLVAVITGAS.....ENPFLNGEYIRLDGAIKMAP 261

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PC1_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PC105_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1304	100.0	261	US-09-931-186-6	Sequence 6, Appl1
2	1290	99.6	261	US-09-931-186-8	Sequence 8, Appl1
3	1290	98.9	261	US-09-931-186-20	Sequence 20, Appl1
4	1289	98.8	261	US-09-931-186-4	Sequence 4, Appl1
5	1289	98.8	261	US-09-931-186-23	Sequence 23, Appl1
6	1287	98.7	261	US-09-931-186-2	Sequence 2, Appl1
7	1136	87.1	227	US-09-984-245-245	Sequence 245, App
8	1136	87.1	227	US-09-986-262-245	Sequence 245, App
9	1136	87.1	227	US-09-983-966-245	Sequence 245, App
10	1136	87.1	227	US-10-433-090-245	Sequence 245, App
11	664.5	51.0	388	US-09-920-923-411	Sequence 411, Appl1
12	332.5	25.5	259	US-09-931-186-17	Sequence 17, Appl1
13	331.5	25.4	243	US-09-815-242-13360	Sequence 13360, A
14	331.5	25.4	243	US-09-815-242-13581	Sequence 13581, A
15	314	24.1	237	US-10-175-096-12	Sequence 14, Appl1
16	314	24.1	237	US-09-823-901-12	Sequence 2, Appl1
17	308.5	23.7	245	US-09-815-242-10921	Sequence 10921, A
18	305.5	23.4	253	US-09-931-186-15	Sequence 15, Appl1
19	301	23.1	247	US-09-479-040-9	Sequence 9, Appl1

20	297.5	22.8	267	US-09-773-748-1	Sequence 1, Appl1
21	292.5	22.4	262	US-10-307-385-6	Sequence 6, Appl1
22	292.5	22.4	262	US-09-802-883-6	Sequence 6, Appl1
23	290.5	22.3	270	US-09-978-295A-468	Sequence 468, App
24	290.5	22.3	270	US-09-978-697-468	Sequence 468, App
25	290.5	22.3	270	US-09-978-192A-468	Sequence 468, App
26	290.5	22.3	270	US-09-999-832A-468	Sequence 468, App
27	290.5	22.3	270	US-09-978-189-468	Sequence 468, App
28	290.5	22.3	270	US-09-978-608A-468	Sequence 468, App
29	290.5	22.3	270	US-09-978-191A-468	Sequence 468, App
30	290.5	22.3	270	US-09-978-403A-468	Sequence 468, App
31	290.5	22.3	270	US-09-978-564A-468	Sequence 468, App
32	290.5	22.3	270	US-09-978-585A-468	Sequence 468, App
33	290.5	22.3	270	US-10-017-081A-468	Sequence 468, App
34	290.5	22.3	270	US-09-978-824-468	Sequence 468, App
35	290.5	22.3	270	US-09-981-915A-468	Sequence 468, App
36	290.5	22.3	270	US-09-999-833A-468	Sequence 468, App
37	290.5	22.3	270	US-10-167-749-468	Sequence 468, App
38	290.5	22.3	270	US-09-918-585A-468	Sequence 468, App
39	290.5	22.3	270	US-09-978-423A-468	Sequence 468, App
40	290.5	22.3	270	US-10-013-921A-468	Sequence 468, App
41	290.5	22.3	270	US-10-013-929A-468	Sequence 468, App
42	290.5	22.3	270	US-10-016-177A-468	Sequence 468, App
43	290.5	22.3	270	US-09-999-830A-468	Sequence 468, App
44	290.5	22.3	270	US-09-978-157A-468	Sequence 468, App
45	290.5	22.3	270	US-09-978-187B-468	Sequence 468, App
46	290.5	22.3	270	US-09-978-643A-468	Sequence 468, App
47	290.5	22.3	270	US-10-166-709A-468	Sequence 468, App
48	290.5	22.3	270	US-09-815-242-10126	Sequence 10126, A
49	289.5	22.2	244	US-09-364-847-6	Sequence 6, Appl1
50	288.5	22.1	246	US-09-364-847-10	Sequence 10, Appl1
51	288.5	22.1	641	US-09-364-847-19	Sequence 19, Appl1
52	288.5	22.1	641	US-09-364-847-51	Sequence 51, Appl1
53	288.5	22.1	642	US-09-364-847-61	Sequence 61, Appl1
54	288.5	22.1	642	US-09-364-847-69	Sequence 69, Appl1
55	285.5	21.9	244	US-09-849-092-13	Sequence 13, Appl1
56	283.5	21.7	203	US-10-175-696-19	Sequence 19, Appl1
57	283.5	21.7	203	US-09-823-901-17	Sequence 7, Appl1
58	278	21.3	263	US-09-815-242-14092	Sequence 14092, A
59	276.5	21.2	254	US-09-978-758-2	Sequence 2, Appl1
60	276	21.0	258	US-09-978-6436	Sequence 6436, App
61	274	21.0	206	US-09-997-816-4	Sequence 4, Appl1
62	272.5	20.9	272	US-09-815-242-12688	Sequence 12688, A
63	271.5	20.8	251	US-09-815-242-5689	Sequence 5689, App
64	268.5	20.6	246	US-09-815-242-5461	Sequence 5461, App
65	268.5	20.6	246	US-09-815-242-12123	Sequence 12123, A
66	268.5	20.6	246	US-09-815-242-12803	Sequence 12803, A
67	268.5	20.6	246	US-09-815-242-13100	Sequence 13100, A
68	268	20.6	251	US-10-272-419-20	Sequence 20, Appl1
69	266.5	20.4	252	US-09-815-242-10974	Sequence 10974, A
70	266.5	20.4	252	US-09-910-033A-2	Sequence 2, Appl1
71	266	20.4	256	US-09-954-114-14	Sequence 14, Appl1
72	266	20.4	285	US-09-815-242-10241	Sequence 10241, A
73	263	20.2	276	US-09-944-160-24	Sequence 24, Appl1
74	262.5	20.1	258	US-10-156-055A-1	Sequence 1, Appl1
75	262.5	20.1	286	US-09-815-242-11860	Sequence 11860, A
76	259	19.9	253	US-09-815-242-11842	Sequence 11842, A
77	257	19.7	261	US-09-971-556-74	Sequence 74, Appl1
78	254	19.5	261	US-09-940-037A-29	Sequence 29, Appl1
79	251.5	19.3	266	US-09-981-383-40	Sequence 40, Appl1
80	251.5	19.3	266	US-09-885-303A-22	Sequence 22, Appl1
81	251.5	19.3	266	US-10-201-823-18	Sequence 18, Appl1
82	251.5	19.3	266	US-09-931-186-18	Sequence 18, Appl1
83	249	19.1	221	US-09-764-853-553	Sequence 553, App
84	243.5	18.7	262	US-09-815-242-10597	Sequence 10597, A
85	242.5	18.6	261	US-09-815-242-10846	Sequence 10846, A
86	242.5	18.6	274	US-09-976-059-17	Sequence 17, Appl1
87	242	18.6	258	US-09-964-314-12	Sequence 12, Appl1
88	239	18.3	251	US-09-922-801-16	Sequence 16, Appl1
89	239	18.3	255	US-09-931-186-14	Sequence 14, Appl1
90	238	18.3	247	US-09-815-242-11893	Sequence 11893, A
91	235	18.0	271	US-09-815-242-13387	Sequence 13387, A
92	235	18.0	272	US-09-815-242-13679	Sequence 13679, A

C:Accession: S22450; S19832
R:Klein, B.; Pawlowski, K.; Hoerliche-Grandpierre, C.; Schell, J.; Toepter, R.
Mol. Gen. Genet. 233: 122-128, 1992
A:Title: Isolation and characterization of a cDNA from *Cuphea lanceolata* encoding a beta
A:Reference number: S22450; MUID:92293104; PMID:1376402
A:Accession: S22450
A:Molecule type: mRNA
A:Residues: 1-320 <KLE>
A:Cross-references: EMBL:X64566; NID:918045; PIDN:CAA45866.1; PID:g18046
A:Experimental source: Immature embryo
C:Genetics:
A:Gene: CLKr27
A:Genome: nuclear
C:Function:
A:Description: EC 1.1.1.100 [validated, MUID:92293104]
A:Pathway: fatty acid biosynthesis
C:Note: Integral part of the fatty acid synthase type II
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: chloroplast; fatty acid biosynthesis; NADP; oxidoreductase
F:1-63/Domain: transit peptide (chloroplast) #status predicted <NP>
F:64-320/Product: 3-oxoacyl-[acyl-carrier-protein] reductase #status predicted <MT>
F:78-255/Domain: short chain alcohol dehydrogenase homology <SADR>
F:127/Active site: Tyr #status predicted

Query Match	25.6%	Score 334	DB 2	Length 320
Best Local Similarity	32.7%	Pred. No. 2,86-18		
Matches	87	Conservative 46	Mismatches 111	Indels 22
			Gaps 6	
QY	2	AAACRSYKGLVAVITGGSGSGGLGATAEKLVGQGSAYVLDPNSNGEA-----QAKIKGN	56	
DB	69	AGAGQSYSPVAVITVIGASRGIGKALATSL-GRAGCKYLVNARSRSKEEVSKEIEAFGG	127	
QY	57	NVAVPAPEADVTESEKDVOTALAKGKFRVDAVAVACAGIAVASKYTNLKKGOTHTLEDFOR	116	
DB	128	QALFEGGVSKEEDYEMAKITAVDAMGVTDVLVNNAGITRGLLMRKMSQ-----WQE	181	
QY	117	VLDVNLAKMTFENVIRLVAGEGQNEPDQGGVGIINTASVAAFEGQVQAAYSASKGIV	176	
DB	182	VIDINTLVGVFCTQAPAAKIMKK-----KKGRILINIASVGLVGNAGQAYSAAKAGVI	235	
QY	177	GMTLPFIARDLAPIGIRVWTIAPGLFGTPIILSLPEKVCNPLASQVFPFSRLGDPAEYVHL	236	
DB	236	GFTTVAAREYASRNINNVAAVAPGFSSDMSEKLDODIKKLEIPIPL-GRYGQEEVAVGL	294	
QY	237	VQALTEHP---FLNGEYVRLDGAIRM	259	
DB	295	VEFLAINPASSYVTGQVFTIDGMITM	320	

RESULT 17
 C833961
 3-oxoacyl-(acyl-carrier protein) reductase fabg [imported] - *Bacillus halodurans* (strain
 C:Species: *Bacillus halodurans*
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 03-Aug-2001
 C:Accession: C833961
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirata,
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A:Reference number: AB6560; MUID:20512582; PMID:11058132.
 A:Accession: C833961
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-246 <STO>
 A:Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDB:BA06210.1; GSPDB:GN000
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: fabg
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

```

QY      8 VKGVAVITIGASLSLATAERLYGQASAVLIDLPLPSGGE-----AQARKLGNVV 59
Db      2 LQGTALVLTGASRIGAPATMELARHGANVY-----NYAGNKEKAENVAEIKELSYEAI 57
QY      60 FAPADVTSEKDVCTALALAKGKFGVDVAVNCAGIAVASFTYLNKKQCHTLEDFORVLD 119
Db      58 ALCQADVDESSEVCAMVKEITLDFEGAVDILVNNAGITPDNLFMRKE-----EDMDAVID 111
QY      120 VNIMGTFENVIRLVANGEGONEPDGQGR-CVIINTASVAPBEGVGQGAASASKGIVGM 178
Db      112 TNLKGIVHCASKATYRPMK-----QRFRIIVSSVYCAIGNAGCANVYAAKAGVIGL 164
QY      179 TLPIARDLAPIGIRVMTIAPGLEFPTLLTSLPEKVCNFLASQVPEPSRLDDPAZYAHLVQ 238
Db      165 TKTLARLARNNTIVNVAAPGFIETDWTGELPEDEVKQMLGQPL-ARLQGPFEVAKAVR 223
QY      239 AIIEN--PFLNGEYIRLDGAI RM 259
Db      224 FLASDDASLYLGGTIIHNGGMM 246

```

RESULT 18
E97919
3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) [Imported] - Streptococcus
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C:Accession: E97919
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczyk, L.; Burett, S.; DeHoff, B.S.
y, R.; Leblanc, D.J.; Lee, L.N.; Leikowitz, E.C.; Lu, J.; Matsushima, F.; McAtreen, S.
y, P.; Sun, P.M.; Winkler, M.E.
U: Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: E97919
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-243 <KDP>
A:Cross-references: GB:AF007317; PIDD:AKA99185.1; PIDD:G15457942; GSPDB:GN00174
A:Genetics:
A:Gene: fadB
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: oxidoreductase

[illegible]

RESULT 10

F83098
Probable short-chain dehydrogenase PA4389 (imported) - *Pseudomonas aeruginosa* (strain PA C) Species: *Pseudomonas aeruginosa*
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C/Accession: F83098
C/Owner: C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B. Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lam, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: F83098
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-252 <STO>
A/Cross-references: GB:AE004854; GB:AE004091; NID:99950606; PIDN:AA07777.1; GSPDB:GN001
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA4389
C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 27.2%; Score 355; DB 2; Length 252;
Best Local Similarity 35.1%; Pred. No. 5.1e-20;

Matches 94; Conservative 40; Mismatches 100; Indels 34; Gaps 7;

QY 8 VKGLAVITGGASGLATAEKLVGOGASAVLDPN-----SGERQAKKLG 55
DB 3 LKDRVITITGGCGGLGAKGKBYLAGKARLALVDLNERLDEAVACKAGGARA--- 58
QY 56 NNVFAPADVTSEKDVOTALAKKRGYDVAVNCAGIAVASKTYNLKRGQTH--TLED 113
DB 59 -----YCNVADDEQVTHMAVAQVSDGALNGLVNNGGILRDGTTIVKRGQSKSLAQ 113
QY 114 FQRLVDNLMGTENVITLVAGEMQ--NEPDGQGRVITINTASVAFEQVGQAASAS 171
DB 114 WQSYIDVNLGVFLCTEYVAKMELNE-----GAIYNTSSISR-AGNMGOANSAA 165
QY 172 KGTIVGMTLPFARDLPFIRKMTIAPGLFTGTPLTSLPEKVCNPLASQVPPSRLDPA 231
DB 166 KAGVAADTVWAKKLAYGIRVAGVAPGFIETEMTACMKPEALEKMTAGIPL-KRMGRPV 224
QY 232 EYAHVQAITEPNFLNGEVIRLDGAIRM 259
DB 225 EIAHSVAYIFENDYYTGTGVLLELDGRL 252

RESULT 11

H72219
3-oxoacyl-(acyl carrier protein) reductase - *Thermotoga maritima* (strain MSB8)

C/Species: *Thermotoga maritima*

C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C/Accession: H72219

R.Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.

Nature 399, 323-329, 1999

A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A/Reference number: A72200; MUID:99287316; PMID:10360571

A/Accession: H72219

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-246 <ARN>

A/Cross-references: GB:AE001811; GB:AE000512; NID:94982291; PIDN:AA036790.1; PID:9498230

A/Experimental source: strain MSB8

C/Genetics:
A/Gene: TM1724
C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F:6-185/Domain: short-chain alcohol dehydrogenase homology <SAD>

Query Match 26.5%; Score 346; DB 2; Length 246;

Best Local Similarity 34.1%; Pred. No. 2.4e-19;
Matches 87; Conservative 47; Mismatches 103; Indels 18; Gaps 5;

QY 8 VKGLAVITGGASGLATAEKLVGOGASAVLDPN-----QAKKGNVVFAPAD 64
DB 3 LEGKCLITIGASGKGNKNTLLFAGEGFTVLAGDSTKENDLSLVEAGLPGKVDPLYLN 62
QY 65 VTSEKDVOTALAKKRGYDVAVNCAGIAVASKTYNLKRGQTHLEDFOYRLDYNLMG 124
DB 63 VYDRQIKKVEKVVQKRGYDVLVNNAGITPDLALVRKE-----EDMDAVIVNVLKG 116
QY 125 TFNVITLVAGEGONEPDGQGRVITINTASVAFEQVGQAASASKGIVGMTLPAR 184
DB 117 VENVITQVYPMIKO-----RNGSLVAVSSVYIGNPGQNTNAAASKAGVGMKTMAK 170
QY 185 DLAPGIRVMTIAPGLFTGTPLTSLPEKVCNPLASQVPPSRLGDPAEYAHLY--QAIT 242
DB 171 ELAGRIRIVNAVAPGFIETPMTKEKPEKARETALSRIPL-GRFGKPEEVAQVILFLASDE 229
QY 243 NFPLNGEVIRLDGAIRM 257
DB 230 STVITGQVIGIDGGL 244

RESULT 12

F97338
3-ketocacyl-acyl carrier protein reductase (imported) - *Clostridium acetobutylicum*

C/Species: *Clostridium acetobutylicum*

C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001

C/Accession: F97338

R.Nollins, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L. J. Bacteriol. 183, 4823-4838, 2001

A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A/Reference number: A96900; MUID:21359325; PMID:21359325

A/Accession: F97338

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-249 <KRU>

A/Cross-references: GB:AE001437; PIDN:AAK81497.1; PID:915026670; GSPDB:GN00168

A/Experimental source: *Clostridium acetobutylicum* ATCC824

C/Genetics:
A/Gene: CAC3574

C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 26.3%; Score 343.5; DB 2; Length 249;

Best Local Similarity 33.2%; Pred. No. 3.9e-19;

Matches 86; Conservative 56; Mismatches 96; Indels 21; Gaps 6;

QY 8 VKGLAVITGGASGLATAEKLVGOGASAVLDPN-----AKKGNVVFAP 62
DB 5 LSGKVAIVVIGAGGLGRALNKLAAEGANLV-VNHSSEAFQKLEIBELGKRAVAVK 63
QY 63 ADVTSEKDVOTALAKKRGYDVAVNCAGIAVASKTYNLKRGQTHLEDFOYRLDYNL 122
DB 64 ADTSKDEMTETIKKALDEGVYDILVNNAGITKMDLPMKE-----EDDSVIVNVL 117
QY 123 MGFNVITLVAGEGONEPDGQGRVITINTASVAFEQVGQAASASKGIVGMTLP 182
DB 118 KGFNCKIKRHSRYMLK-----KSKITINISSVIGLIGNAGOVNAAAKAGIGTKVAY 171
QY 183 ARDLAPGIRVMTIAPGLFTGTPLTSLPEKVCNPLASQVPPSRLGDPAEYAHLY 242
DB 172 AKELASRGITVNAVAGIISDMTDLTDKORSIVAAYPL-NKVGAEADVAVNLVFLAS 230
QY 243 --NFPLNGEVIRLDGAIRM 259
DB 231 DLSSTITGQVITVNDGAVK 249

RESULT 13

T51084
3-oxoacyl-(acyl carrier protein)-reductase (oar-1) (imported) - *Neurospora crassa*

Db 238 NDYMGVIRLDGAIKMP 256

RESULT 7

AG2750

3-hydroxyacyl-CoA dehydrogenase type II Atu1415 [imported] - Agrobacterium tumefaciens C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002

C:Accession: AG2750

R:Wood, D.W.; Seubald, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kulyavin, T.; Levy, R.; Li, M.; McClellan, S.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kulyavin, T.; Levy, R.; Li, M.; McClellan, S. Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.E.W.

A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AG2750

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-257 <KUR>

A:Cross-references: GB:AE00688; PIDN:AL42421.1; PID:q1773983; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu1415

A:Map position: circular chromosome

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 49.2%; Score 642; DB 2; Length 257;

Best Local Similarity 51.7%; Pred. No. 5.2e-42;

Matches 134; Conservative 41; Mismatches 76; Indels 8; Gaps 3;

QY 7 SVKGIIVITGGAGGLIATERYVGQASAVLLDPSNGEQAOKLGNVVPADYV 66

Db 2 NIEGAGALVTGAAGLGAARMAARAAATITDRNGEKKLAIEIGRAV--GGDVT 59

QY 67 SEKDQVTLALAKGFGVDVAVNCAGIAVASKTYNKKGGTHTLEFQRYLDVNLGTE 126

Db 60 SDADQAAIKVAASAKGSLRLVNCAGIGTAGRI--LGRBPQPLGSEFGYIRNLIGTF 117

QY 127 NVIRLVAGMGQNEPDG---GGRGVITNTASVAAFEGVGOAAYSASKGGIYGMPLT 182

Db 118 NMRLAAAHMAEREDGSDRQDNGVTVNTASVAAFEGQICGAAYASAKGGIYSLALPA 177

QY 183 ARDLAPIGIRVMTAPGLFGTPLTSLPEKVCNLTASQVPPSRLLGPAEVAHLYQAITE 242

Db 178 ARELARFRIRVNTVAPGIFLTPILQGLPQEVQESLAGQIRHPSRLGDPAEFADIVRELI 237

QY 243 NPELVGEVIRLDGAIKMP 261

Db 238 NDYMGVIRLDGAIKMP 256

RESULT 8

CG7264

3-hydroxyacyl-CoA dehydrogenase [imported] - Caulobacter crescentus C:Species: Caulobacter crescentus

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C:Accession: CG7264

R:Niemann, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Klotz, N.; J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete genome sequence of Caulobacter crescentus.

A:Reference number: AB7249; MUID:21173698; PMID:11259647

A:Accession: CG7264

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-260 <STO>

A:Cross-references: GB:AE005673; NID:q13421233; PIDN:AAK22111.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC0124

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 45.6%; Score 595; DB 2; Length 260;

Best Local Similarity 51.0%; Pred. No. 2.1e-38;

Matches 130; Conservative 30; Mismatches 89; Indels 6; Gaps 2;

QY 11 LVAVITGGAGGLIATERYVGQASAVLLDPSNGEQAOKLGNVVPADYTSKD 70

Db 7 VAAVITGGAGGLIATERYVGQASAVLLDPSNGEQAOKLGNVVPADYTSKD 64

QY 71 VQTALALAKGFGVDVAVNCAGIAVASKTYNKKGGTHTLEFQRYLDVNLGTE 126

Db 65 VAGEKRAAAGQERILVNCAGITNNAKTASRDATGETHNPILDADRIIQILVQTF 124

QY 127 NVIRLVAGMGQNEPDGQGRGVITNTASVAAFEGVGOAAYSASKGGIYGMPLT 186

Db 125 RCIASAKGMLDLEPLEDGERGAIIVTASVAEDQOMQAAVSASKGGVGMPLIARDL 184

QY 187 APGIRVMTIAPGLFGTPLTSLPEKVCNLTASQVPPSRLLGPAEVAHLYQAITE 246

Db 185 MGEIRVMTIAPGLFGTPLTSLPEKVCNLTASQVPPSRLLGPAEVAHLYQAITE 244

QY 247 NGEVIRLDGAIKMP 261

Db 245 NGEVIRLDGAIKMP 259

RESULT 9

E70740

probable fabG2 protein - Mycobacterium tuberculosis (strain H37RV) C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: E70740

R:Coole, S.T.; Broesch, R.; Parthill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R.; Connor, R.; Davies, R.; Devlin, K.; Pattwell, T.; Gentles, S.; Hamilton, N.; Holroyd, R.; Andream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome.

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: E70740

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-247 <COL>

A:Cross-references: GB:275555; GB:AL123456; NID:q3261608; PIDN:CAA99983.1; PID:q14190

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: fabG2

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

F:8-186/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 29.4%; Score 383.5; DB 2; Length 247;

Best Local Similarity 38.9%; Pred. No. 3.3e-22;

Matches 96; Conservative 43; Mismatches 91; Indels 17; Gaps 5;

QY 13 AVITGGAGGLIATERYVGQASAVLLDPSNGEQAOKLGNVVPADYTSKD 70

Db 10 AVITGGAGGLIATERYVGQASAVLLDPSNGEQAOKLGNVVPADYTSKD 69

QY 71 VQTALALAKGFGVDVAVNCAGIAVASKTYNKKGGTHTLEFQRYLDVNLGTE 130

Db 70 VDLIRVAVRFGGLDVMVNAITRDATV---RTMEEFDVIAVHLKGTNGTR 123

QY 131 LVAGMGQNEPDGQGRGVITNTASVAAFEGVGOAAYSASKGGIYGMPLIARDLAPIG 190

Db 124 LAALIMR-----KGAIVNNSVSGKGMVGTNTSASAKGIGMTAAKELAHLG 177

QY 191 IRVMTIAPGLFGTPLTSLPEKVCNLTASQVPPSRLLGPAEVAHLYQAITE--NPLNG 248

Db 178 IRVMTIAPGLIRSMTEAMPQRIWDOKLAIEVPM-GRAGESEVASAVFLASDLSSYMG 236

QY 249 EVIRLDG 255

Db 237 TVLDVGT 243

[illegible]

C:Genetics:
A:gene: RV1144
C:superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F:6-187/domain: short-chain alcohol dehydrogenase homology <SAD>

Query Match 51.5%; Score 671.5; DB 2; Length 250;
Best Local Similarity 60.1%; Pred. No. 2.8e-44;
Matches 152; Conservative 25; Mismatches 69; Indels 7; Gaps 4;

QY 9 KGLVAVITGGASGIGLTAERLVGQASAVYLDPNSGGEAOAKKIGNNVFAADVTSE 68
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 4 KDAAVAAYTGGASGIGLATRKRLDLAGQVVYVD---RGDDVYGGLDRARFPQADVTE 60
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 69 KDVOPTALALAKGKFRVDVAVNCAGIAVASKTIVLKKGOTHTLEDFOVLVDNLMTFFNY 128
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 61 AAASNALELA-DSLGPVRYVVCAGTGNNARV--LSRDGVFLPAEFRIVDINVGTFNY 117
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 129 IRIVAGEHGNPEPPOGGRGVIINTASVAAPREGOVGAASASAKGIYGMTPIARDLPAR 188
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 118 LRLGAERIARKEP-IGBERGYIINTASVAAPDGGICGAASASAKGVGMGLPIARDLAS 176
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 189 IGIRVMYTPGLFGTPLITSLEPKVCNFLLSQVPFSPSLGDPAEYAHLYOATINPFLNG 248
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 177 KLIRVYTATPOLFTPTPLIASLPAEAARKSGOOVPHPSLGNDPEXGALVHLIEPNMLNG 236
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 249 EVIRLDGAIKMP 261
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 237 EVIRLDGAIKMAP 249
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 6
F97531.
probable short-chain dehydrogenase (P22554) [imported] - Agrobacterium tumefaciens (s
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: F97531
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirollo, B.; Goldm
A.: Liu, F.; Molim, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2333-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A:Reference number: AF9359; PMID:11743194
A:Status: Preliminary
A:Accession: F97531
A:Molecule type: DNA
A:Residues: 1-257 <KUP>
A:Cross-references: GB:AE007869; PIDN:AAR87207.1; PID:g15156487; GSPDB:GN00169
C:Genetics:
A:gene: AGR_C_2613
A:Map position: Circular chromosome
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 49.2%; Score 642; DB 2; Length 257;
Best Local Similarity 51.7%; Pred. No. 5.2e-42;
Matches 134; Conservative 41; Mismatches 76; Indels 8; Gaps 3;

QY 7 SVKGLVAVITGGASGIGLTAERLVGQASAVYLDLPNSGGEAOAKKIGNNVFAPADVT 66
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 2 NTEGAGALTGGAASGIGAARMLARQAAYTIFDRNGEAGKKLAETGKRAV--QGDTV 59
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 67 SEKDVOTALAKKGFGRVDVANCGIAVASKTYLNKKGOTHTLEDFORYLDVNLMKGT 126
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 60 SOADAQAAMIKVAASAKGGRILYNAGIGTAGRI-LDREGQPQLGDEQYIVRVLTCTF 117
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 127 NVIRLVAGEMGNEDDG---GORGVIINTASVAAPFEQGVQQAAYSMSKSGIVMTLPI 182
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 118 NMNRILAAAAMAREDEDGDSQRDNQGVYVNTASVAAPFGQIGQAAYASKSIGTISLAPA 177
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 183 ARDLAPICIRVYTIAPGLFTPLTSLEPKCNFLASGVPPSRSLGDAEYAHLYOATIE 242
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 178 ARELARFRIRVYTIAPGLFTPLTGLQPOEVGESLAGGIIPHSRSLGDAEFADTVRFIE 237
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 243 NEPLINGEVIRLDGAIKMP 261
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

ALIGNMENTS

RESULT 1

T20484

hypothetical protein F01G4.2 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000

C:Accession: T20484

R: Harris, B.

submitted to the EMBL Data Library, January 1996

A:Reference number: Z19281

A:Accession: T20484

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-258 <MIL>

A:Cross-References: EMBL:Z68341; PIDN:CAA92764.1; GSPDB:GN00022; CESP:F01G4.2

A:Experimental source: clone F01G4

C:Genetics:

A:Gene: CESP:F01G4.2

A:Map position: 4

A:Intons: 8/3; 116/3; 162/3; 209/3

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 57.4%; Score 748; DB 2; Length 258;

Best Local Similarity 59.9%; Pred. No. 3.9e-50;

Matches 154; Conservative 34; Mismatches 67; Indels 2; Gaps 1;

QY 3 AACRSYKGVAVITGGASGLGATAEKLVGOGASAVLLDLPNSGGEPAOKKIGNNVFAP 62
 DB 2 SALRSTKGLVALVTGASGLGCAFAEVLAKAGQVAIIDLPKSGADVAKEIG--ITFP 59
 QY 63 ADVTSEKDVQATALAKKFGKRVAVAVNCAGIYAVSKTYNKKGOTHTLEDFORVLDVNL 122
 DB 60 ASYTSSEEVAAFAKQVAEGRLDALVNCAGIYAFKLYSVCKKHVDFEKKIRQITDVNV 119
 QY 123 MGFNTYIRLVAGMGONPEPDGSGRGVITNTASVAAFEGOVGOAAVSASKGGIVGKTIPI 182
 DB 120 LGFTNFYIRHGVNLMGHEKDAQNGQKQVYINTASVAAPDQTOQSASAKGAIYGMTLPL 179
 QY 183 ARDLAPIGIRVMTIAGLFTGTPLLTSLPEKVCNFTLASQVFPFSRLGDPAEVAHLVQALTE 242
 DB 180 ARDFAGGIRFNTIAGLMDTPIILSLPEKVSFLAQLIPNSRLGHPHEGALVQHTE 239
 QY 243 NPFLNGEVIRLDGAIKM 259
 DB 240 NQYLNGETTIRFDGALRM 256

RESULT 2

H83326

Probable short-chain dehydrogenase PA2554 [imported] - *Pseudomonas aeruginosa* (strain P)C:Species: *Pseudomonas aeruginosa*

C:date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: H83326

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lam,

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A:Reference number: A82950; MIMD:20457337; PMID:10984043

A:Accession: H83326

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-255 <STO>

A:Cross-References: GB:AE004683; GB:AE004091; NID:999448607; PIDN:AA05942.1; GSPDB:GN001

C:Genetics:

A:Experimental source: strain PA01

A:Gene: PA2554

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 54.5%; Score 711; DB 2; Length 255;

Best Local Similarity 57.1%; Pred. No. 2.7e-47;

Matches 144; Conservative 37; Mismatches 69; Indels 2; Gaps 1;

QY 8 VKGLVAVITGGASGLGATAEKLVGOGASAVLLDLPNSGGEPAOKKIGNNVFAPADVT 67
 DB 3 IENRFVLTGGSSGLGATAEKLVGOGASAVLLDLPNSGGEPAOKKIGNNVFAPADVT 62
 QY 68 EKDVOFTALAKKFGKRVAVAVNCAGIYAVSKTYNKKGOTHTLEDFORVLDVNLGTFN 127
 DB 63 DTDGFAATAAAIEAFSRDVLVNCAGVAPGKRV--LGEGAHKKEITRTISIMLSTFN 120
 QY 128 VTRLVAGMGONPEPDGSGRGVITNTASVAAFEGOVGOAAVSASKGGIVGKTIPIARDIA 187
 DB 121 MLRLAEMAMNNEPQSGERGVIYNTASVAAPDQTOQSASAKGAIYGMTLPLVARELA 180
 QY 188 PIGIRVMTIAGLFTGTPLLTSLPEKVCNFTLASQVFPFSRLGDPAEVAHLVQALTEPFLN 247
 DB 181 RFGIRVMTIAGLFTGTPLLTSLPEKVCNFTLASQVFPFSRLGDPAEVAHLVQALTEPFLN 240
 QY 248 GEVIRLDGAIKM 259
 DB 241 GEVIRLDGAIKM 252

RESULT 3

AG3611

3-oxoacyl-(acyl-carrier protein) reductase (EC 1.1.1.100) [imported] - *Brucella melit*C:Species: *Brucella melitensis*

C:date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002

C:Accession: AG3611

R:DeVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanov

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melit*

A:Reference number: AD3352; PMID:11756688

A:Accession: AG3611

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-255 <KUN>

A:Cross-References: GB:AE008918; PIDN:AAU54058.1; PID:917985013; GSPDB:GN00191

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME10816

A:Map position: 11

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C:Keywords: oxidoreductase

Query Match 57.1%; Score 711; DB 2; Length 255;

Best Local Similarity 57.1%; Pred. No. 2.7e-47;

Matches 144; Conservative 37; Mismatches 69; Indels 2; Gaps 1;

QY 8 VKGLVAVITGGASGLGATAEKLVGOGASAVLLDLPNSGGEPAOKKIGNNVFAPADVT 67
 DB 3 IENRFVLTGGSSGLGATAEKLVGOGASAVLLDLPNSGGEPAOKKIGNNVFAPADVT 62
 QY 68 EKDVOFTALAKKFGKRVAVAVNCAGIYAVSKTYNKKGOTHTLEDFORVLDVNLGTFN 127
 DB 63 DTDGFAATAAAIEAFSRDVLVNCAGVAPGKRV--LGEGAHKKEITRTISIMLSTFN 120
 QY 128 VTRLVAGMGONPEPDGSGRGVITNTASVAAFEGOVGOAAVSASKGGIVGKTIPIARDIA 187
 DB 121 MLRLAEMAMNNEPQSGERGVIYNTASVAAPDQTOQSASAKGAIYGMTLPLVARELA 180
 QY 188 PIGIRVMTIAGLFTGTPLLTSLPEKVCNFTLASQVFPFSRLGDPAEVAHLVQALTEPFLN 247
 DB 181 RFGIRVMTIAGLFTGTPLLTSLPEKVCNFTLASQVFPFSRLGDPAEVAHLVQALTEPFLN 240
 QY 248 GEVIRLDGAIKM 259
 DB 241 GEVIRLDGAIKM 252

RESULT 4

H95360

3-oxoacyl-(acyl-carrier protein) reductase (EC 1.1.1.100) [imported] - *Brucella melit*C:Species: *Brucella melitensis*

C:date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002

C:Accession: H95360

R:DeVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanov

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melit*

A:Reference number: AD3352; PMID:11756688

A:Accession: H95360

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-255 <KUN>

A:Cross-References: GB:AE008918; PIDN:AAU54058.1; PID:917985013; GSPDB:GN00191

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME10816

A:Map position: 11

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C:Keywords: oxidoreductase

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 14:23:47 ; Search time 15.6667 Seconds

(Without alignments)
1601.559 Million cell updates/sec

Title: US-09-931-186-6

Perfect score: 1304
Sequence: 1 MAACRSVKGLVAVITGAS.....ENPFNGEVI RLDGAI RMP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR.73.*
2: PIR1.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	748	57.4	258	2 T20484	hypothetical prote
2	720	55.2	258	2 H83326	probable short-cha
3	711	54.5	255	2 AG3611	3-oxoacyl-(acyl-ca
4	675	51.8	255	2 H95380	Probable [imported
5	671.5	51.5	250	2 A70554	Probable dehydroge
6	642	49.2	257	2 F97531	Probable short-cha
7	642	49.2	257	2 AG2750	3-hydroxyacyl-CoA
8	595	45.6	260	2 C87264	3-hydroxyacyl-CoA
9	383.5	29.4	247	2 E70740	probable fabG2 pro
10	355	27.2	252	2 F83098	Probable short-cha
11	346	26.5	246	2 H72219	3-oxoacyl-(acyl ca
12	343.5	26.3	246	2 F97358	3-oxoacyl-(acyl ca
13	340.5	26.1	297	2 T51084	3-oxoacyl-(acyl-ca
14	335	25.7	246	2 H84136	3-oxoacyl-(acyl-ca
15	334.5	25.7	251	2 AH2042	3-oxoacyl-(acyl-ca
16	334	25.6	320	2 S22450	3-oxoacyl-(acyl-ca
17	333.5	25.4	246	2 C83961	3-oxoacyl-(acyl-ca
18	331.5	25.4	243	2 E97293	3-oxoacyl-(acyl-ca
19	330.5	25.3	243	2 G95048	3-oxoacyl-(acyl-ca
20	328.5	25.2	248	2 F82128	3-oxoacyl-(acyl-ca
21	324.5	24.9	243	2 F86721	hypothetical prote
22	324.5	24.9	260	2 T36846	Probable dehydroge
23	316.5	24.3	259	2 H98137	3-oxoacyl-(acyl-ca
24	316.5	24.3	296	2 A13149	3-oxoacyl-(acyl-ca
25	316.5	24.3	296	2 E87260	hypothetical prote
26	316	24.2	299	2 D90481	hypothetical prote
27	313.5	24.0	247	2 S77280	3-oxoacyl-(acyl-ca
28	313.5	24.0	260	1 A48154	short-chain alcoh
29	313	24.0	247	2 F82776	3-oxoacyl-(acyl re

30	312.5	24.0	240	2 H75014	3-oxoacyl-(acyl-ca
31	311	23.8	242	2 AB3545	toluenesulfonate z
32	310	23.8	249	2 AG3121	dehydrogenase Atu4
33	310	23.8	253	2 H98165	3-oxoacyl-(acyl-ca
34	310	23.8	267	2 T11579	probable short cha
35	309.5	23.7	244	2 AB0195	3-oxoacyl-(acyl-ca
36	309.5	23.7	246	2 A69621	3-oxoacyl-(acyl-ca
37	308.5	23.7	247	2 AG1300	3-ketoacyl-acyl ca
38	306.5	23.5	247	2 AG1672	3-ketoacyl-acyl ca
39	306	23.5	256	2 A10406	probable dehydroge
40	305	23.4	250	2 S47054	probable dehydroge
41	305	23.4	260	2 H70758	probable fabG3 pro
42	303	23.2	248	2 H98258	3-oxoacyl-(acyl-ca
43	303	23.2	248	2 A13025	3-oxoacyl-(acyl-ca
44	301	23.1	255	2 S39737	glucose 1-dehydrog
45	300.5	23.0	296	2 T26723	hypothetical prote
46	300	23.0	245	2 AE3517	3-oxoacyl-(acyl ca
47	300	23.0	252	2 B90495	hypothetical prote
48	299	22.9	255	2 S10707	20beta-hydroxyster
49	296.5	22.7	258	2 C70885	probable dehydroge
50	294	22.5	255	2 H84288	3-oxoacyl-(acyl-ca
51	294	22.5	265	2 T36396	probable short cha
52	293	22.5	249	1 B37762	bile acid 7-dehydr
53	292.5	22.4	303	2 T46064	short-chain alcoh
54	291.5	22.4	244	2 T12051	3-oxoacyl-(acyl-ca
55	291.5	22.4	248	2 H70447	3-oxoacyl-(acyl-ca
56	290	22.2	258	2 D95284	probable [imported
57	290	22.2	272	2 AG3359	glucose 1-dehydrog
58	289.5	22.2	244	1 B42147	3-oxoacyl-(acyl-ca
59	289.5	22.2	256	1 E72427	oxidoreductase, sh
60	288.5	22.1	246	1 RDA1AE	acetoacetyl-CoA re
61	286.5	22.0	244	2 G90812	3-oxoacyl-(acyl-ca
62	286.5	22.0	244	2 C85672	3-oxoacyl-(acyl-ca
63	285.5	21.9	254	2 G75333	3-oxoacyl-acyl car
64	285	21.9	255	2 G82644	2,5-dichloro-2,5-c
65	284.5	21.8	248	2 E81695	3-oxoacyl-(acyl ca
66	284.5	21.8	257	2 A72395	oxidoreductase, sh
67	284	21.8	240	2 F87312	acetoacetyl-CoA re
68	283.5	21.7	244	2 AD0642	3-oxoacyl-(acyl-ca
69	282.5	21.7	246	1 DEKONG	acetoacetyl-CoA re
70	282.5	21.7	253	2 B86737	acetoin dehydrogen
71	282.5	21.7	272	2 A99950	hypothetical prote
72	282.5	21.7	251	2 C87474	hypothetical prote
73	282	21.6	255	2 D72377	oxidoreductase, sh
74	282	21.6	260	2 F82954	probable short-cha
75	279.5	21.4	241	1 S06998	acetoacetyl-CoA re
76	279	21.4	246	1 S28279	acetoacetyl-CoA re
77	279	21.4	258	2 B89773	acetoal(diacetyl)r
78	278	21.3	263	2 AB0812	probable oxidoredu
79	277	21.2	249	1 A31841	bile acid dehydrox
80	277	21.2	262	2 B97588	oxidoreductase, sh
81	277	21.2	262	2 AG2809	short chain dehydr
82	276.5	21.2	248	2 T44361	acetoacetyl-CoA re
83	275.5	21.1	248	2 F71538	probable oxoacyl (
84	275	21.1	267	2 B87578	hypothetical prote
85	274.5	21.1	248	2 B97223	probable 3-ketoacy
86	274	21.0	259	2 E95903	probable oxidoredu
87	274	21.0	268	2 G96016	probable gluconate
88	272.5	20.9	344	2 T44434	3-oxoacyl-(acyl-ca
89	272.5	20.9	242	2 A47542	short-chain alcoh
90	272	20.9	251	2 G72389	oxidoreductase, sh
91	272	20.9	263	2 S01227	glucose 1-dehydrog
92	272	20.9	319	2 S22416	3-oxoacyl-(acyl-ca
93	270.5	20.7	240	2 S75021	3-xetoacyl-acyl ca
94	270.5	20.7	261	2 S54815	uridymycin polyketi
95	270.5	20.7	262	2 D97325	3-oxoacyl-acyl car
96	269.5	20.7	260	2 G87408	glucanate 5-dehydr
97	269.5	20.7	261	1 S25079	monensin polyketid
98	269.5	20.7	261	2 C91254	probable sorbitol-
99	269	20.6	258	2 T51764	probable 2-hydroxy
100	269	20.6	257	2 F95284	probable [imported

Db 124 CSAVI-----RPMIKARSGAIYNISIVGLRSGSPGQTNAAKAGIIGESKALSKEVGS 177
QY 189 IGIRVMTIAPGLFGTPLLTSLPKVCNFIASQVFPSPRLGDPAE--YAHIVQAIINPFL 246
Db 178 KNIRVNCIAPGFIDTDMTKGLSDNKNEMLKGVPL-GRVGTPEIAMAALFLASNOSYI 236
QY 247 NGEVIRLDGAI 257
Db 237 TGOVLSTVDGGM 247

Search completed: June 23, 2003, 14:29:23
Job time : 9.8333 secs

QY 234 AHLVCAIENP---FLNGEYIRLDGAI RM 260
 ||| : : : | : : :
 Db 222 AHLCVFLADEKRGKITGTGNEIYDGMATK 251

 RESULT 24
 PHBB_ALCEU STANDARD; PRT; 246 AA.
 ID PHBB_ALCEU
 AC P14697;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetoacetyl-CoA reductase (EC 1.1.1.36).
 GN PHBB.
 OS Alcaligenes eutrophus (Ralstonia eutropha).
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 OX NCBI_TaxID=510;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H16 / DSM 428 / ATCC 17689;
 RX MEDLINE=89359356; PubMed=2670935;
 RA Peoples O.P., Sinskey A.U.;
 RT "Poly-beta-hydroxybutyrate biosynthesis in Alcaligenes eutrophus H16.
 RT Characterization of the genes encoding beta-ketothiolase and
 RT acetoacetyl-CoA reductase."
 RL J. Biol. Chem. 264:15293-15297(1989).
 CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxyacyl-CoA + NADP(+) = 3-oxoacyl-CoA + NADPH.
 CC -1- PATHWAY: Poly-beta-hydroxybutyrate biosynthesis; second step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J04987; AAA21973.1; -
 DR PIR: B34340; RDLALAE.
 DR HSP: O70351; IE3S.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR OXidoreductase; NADP; PHB biosynthesis.
 FT NP_BIND 8 32 NADP (BY SIMILARITY).
 FT ACT_SITE 153 153 BY SIMILARITY.
 SQ SEQUENCE 246 AA; 26370 MW; AD6739E0F5C93C06 CRC64;

 Query Match 22.1%; Score 288.5; DB 1; Length 246;
 Best Local Similarity 31.9%; Pred. No. 4,7e-15;
 Matches 81; Conservative 45; Mismatches 109; Indels 19; Gaps 7;

Db 173 TRGVTVNTVSPGYIATDWAKAIRDVDLKIIVATIPV-KRLGLPEIASIACAMLSSESGF 231
 QY 246 LNGEYIRLDGAI RM 259
 ||| : : : | : : :
 Db 232 STGADFSIINGGLIM 245

 RESULT 25
 FABG_CHLMU STANDARD; PRT; 248 AA.
 ID FABG_CHLMU
 AC O9PKE7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
 DE acyl carrier protein reductase).
 GN FABG OR TC0508.
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOPn / N199;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.R., Peterson J., Ulfarback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouli H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MOPn and Chlamydia
 RT pneumoniae AR39."
 RL Nucleic Acids Res. 28:1397-1406(2000).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AE002319; AAF39350.1; -
 DR HSP: P50163; ZAEI.
 DR TIGR: TC0508; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 12 36 NADP (BY SIMILARITY).
 FT ACT_SITE 157 157 BY SIMILARITY.
 SQ SEQUENCE 248 AA; 25977 MW; 1F5C8968CB05FF58 CRC64;

 Query Match 21.8%; Score 284.5; DB 1; Length 248;
 Best Local Similarity 29.1%; Pred. No. 9,5e-15;
 Matches 73; Conservative 48; Mismatches 111; Indels 19; Gaps 5;

RC STRAIN-K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Hojo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimura K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki Y., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiuchi T.;
 RT "A 718-kb DNA sequence of the *Escherichia coli* K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155(1996)
 CC -1- CATALYTIC ACTIVITY: (2R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) -> 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; M84991; AAA23739.1; -
 DR EMBL; AE000210; AAC74177.1; -
 DR EMBL; D90745; BAA35901.1; -
 DR PIR; B42147; B42147.
 DR HSSP; P29132; IDFI.
 DR Ecogene; EG1318; fabG.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 10 34 NADP (BY SIMILARITY).
 FT ACT_SITE 151 151 BY SIMILARITY.
 FT CONFLICT 30 30 A->G (IN REF. 1).
 FT SEQUENCE 244 AA; 25560 MW; 48ECLF2A7F7EEF93 CRC64;
 SQ
 Query Match 22.2%; Score 289.5; DB 1; Length 244;
 Best Local Similarity 30.0%; Pred. No. 3.9e-15;
 Matches 76; Conservative 50; Mismatches 112; Indels 15; Gaps 4;

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative oxidoreductase TM0019 (EC 1.-.-.-).
 GN TM0019.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
 OC Thermotogaceae; Thermotoga.
 NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=96125254; PubMed=8550425;
 RA Kletzin A., Adams M.;
 RT "Molecular and phylogenetic characterization of pyruvate and 2-
 RT ketosovalerate ferredoxin oxidoreductases from *Pyrococcus furiosus*
 RT and pyruvate ferredoxin oxidoreductase from *Thermotoga maritima*.";
 RL J. Bacteriol. 178:248-257(1996).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=9287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.W., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.K.;
 RT Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequence of *Thermotoga maritima*.
 RL Nature 393:323-329(1999).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; X85171; CA59459.1; -
 DR EMBL; AE001690; AAD35113.1; -
 DR HSSP; O70351; 1E6W.
 DR TIGR; TM0019;
 DR InterPro: IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 KW Hypothetical protein; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 9 33 NADP (BY SIMILARITY).
 FT ACT_SITE 153 153 RGGGVIT -> TRWRSDH (IN REF. 1).
 FT CONFLICT 130 136
 FT SEQUENCE 256 AA; 28078 MW; D68160B1D7980C6B CRC64;
 SQ
 Query Match 22.2%; Score 289.5; DB 1; Length 256;
 Best Local Similarity 31.1%; Pred. No. 4.1e-15;
 Matches 84; Conservative 45; Mismatches 104; Indels 37; Gaps 8;

QY 243 NPELNGEVIRLDG 255
 Db 229 SSVYTCAGELAYDGS 241

RESULT 17
 Y4VI_RHISN STANDARD; PRT; 548 AA.
 AC 053217;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Putative short-chain type dehydrogenase/reductase Y4VI (EC 1.-.-.-).
 GN Y4VI.
 OS Rhizobium sp. (strain NGR234).
 OC Plasmid sym PNCGR234.
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Rhizobiaceae; Rhizobium.
 CX NCBI_TaxID=394;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97305956; PubMed=9163424;
 RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
 RA Perret X.;
 RT "Molecular basis of symbiosis between Rhizobium and legumes."; a
 RT Genome Res. 6:590-600(1996).
 RL Nature 387:394-401(1997).
 [2]
 RT "SEQUENCE FROM N.A."
 RA MEDLINE=96389014; PubMed=8796346;
 RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
 RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
 RT NGR234 using dye terminators and a thermostable 'sequenase'"; a
 RT Genome Res. 6:590-600(1996).
 RL -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY. CONTAINS TWO DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z68203; CA92424.1; ALT_INIT.
 DR EMBL; AE000101; AAB91897.1; -
 DR HSSP; P50163; ZAE1.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.2.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
 KW Multifunctional enzyme.
 FT DOMAIN 1 250 SHORT-CHAIN DEHYDROGENASE/REDUCTASE 1.
 FT NP_BIND 12 37 NAD OR NADP (BY SIMILARITY).
 FT ACT_SITE 154 154 BY SIMILARITY.
 FT NP_BIND 280 304 NAD OR NADP (BY SIMILARITY).
 FT ACT_SITE 420 420 BY SIMILARITY.
 SQ SEQUENCE 548 AA; 57593 MW; 393958C5DF17C23F CRC64;

Query Match 22.6%; Score 294.5; Db 1; Length 548;
 Best Local Similarity 33.6%; Pred. No. 4.1e-15;
 Matches 86; Conservative 41; Mismatches 100; Indels 29; Gaps 8;

QY 10 GIVAVITGGASGLAERLVOGASAVYLDLPNSGGEQAKRLGNVFAADYTSER 65
 Db 9 GRTVTVVGAAGGIGRALVYDIFPANGDVYAVDLPDSGVITLGNLGPFGHLEVDVSRED 68

QY 70 DVCTALALANGKFGRTDVAVNCAGI-----AVASKTYLKKKGQHTLEDQFQVLDVNLMT 125
 Db 69 DVVALRALLEKRFRSRIEVLVNNMGITGMATADT-----ALEDFQALAINLYGA 119

QY 126 FNVIRLVAGENGONPPDGGGORGVIINTASVAFEGVGGAAYASAKGIWGLTPIARD 185
 Db 120 YSVACETAKLM---KPG-----AAIVNVAISLGLGNPKRSAYASAKGLISIRKSLACR 171

QY 186 LAPICIRMTATAPGLFGPRLITSPEKY-----CNFLASQVFPFPRRLDPAEYALYQ--A 239
 Db 172 WASRGIRTVAAVPGVFRVPAEEL-ERAKLIDVSAIRRVPL-GRIARPDEIARAVRELA 229

QY 240 IIEPFLNGEVIRLDG 255
 Db 230 SAQASYINGSLVYDGS 245

RESULT 18
 BA71_EUBSP STANDARD; PRT; 249 AA.
 ID BA71_EUBSP
 AC P07914;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 7-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159) (Bile acid
 DE 7-dehydroxylase) (7-alpha-HSDH) (Bile acid-inducible protein).
 GN BA1A1 AND BA1A3.
 OS Eubacterium sp. (strain VPI 12708).
 CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 CC Clostridium.
 CX NCBI_TaxID=29347;
 RN [1]
 RP SEQUENCE FROM N.A. (BA1A3).
 RA MEDLINE=90330548; PubMed=2376563;
 RA Gopal-Srivastava R., Mallonee D.H., White W.B., Hylemon P.B.;
 RT "Multiple copies of a bile acid-inducible gene in Eubacterium sp.
 RT strain VPI 12708.";
 RT J. Bacteriol. 172:4420-4426(1990).
 RL [2]
 RP SEQUENCE FROM N.A. (BA1A1).
 RA MEDLINE=88197993; PubMed=2834320;
 RA Coleman J.P., White W.B., Lijewski M., Hylemon P.B.;
 RT "Nucleotide sequence and regulation of a gene involved in bile acid
 RT 7-dehydroxylation by Eubacterium sp. strain VPI 12708.";
 RT J. Bacteriol. 170:2070-2077(1988).
 RN [3]
 RP SEQUENCE OF 1-55 FROM N.A. (BA1A1), AND SEQUENCE OF 1-33.
 RX MEDLINE=87165759; PubMed=3549693;
 RX Coleman J.P., White W.B., Hylemon P.B.;
 RT "Molecular cloning of bile acid 7-dehydroxylase from Eubacterium sp.
 RT strain VPI 12708.";
 RT J. Bacteriol. 169:1516-1521(1987).
 RL -1- FUNCTION: 7-ALPHA-DEHYDROXYLATION OF CHOLIC ACID, YIELDING
 CC DEOXYCHOLIC ACID AND LITHOCHOLIC ACID, RESPECTIVELY. HIGHEST
 CC AFFINITY WITH TAUROCHENODEOXYCHOLIC ACID.
 CC -1- CATALYTIC ACTIVITY: 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-
 CC cholanate + NAD(+) = 3-alpha,12-alpha-dihydroxy-7-oxo-5-beta-
 CC cholanate + NADH.
 CC -1- PATHWAY: Bile acid catabolism.
 CC -1- INDUCTION: PRESENCE OF C(24) BILE ACIDS CONTAINING A
 CC 7-ALPHA-HYDROXY GROUP.
 CC -1- SIMILARITY: THERE ARE THREE GENES FOR BA1A PROTEINS. BA1A1 IS
 CC IDENTICAL TO BA1A3 AND THERE IS 81% IDENTITY WITH BA1A2.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M34658; AAB61155.1; -
 DR EMBL; M19654; AAB61154.1; -
 DR EMBL; M15813; AAB61153.1; -

RX MEDLINE=98044033; PubMed=9384377;
 RA Kunze F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azavedo J., Bertero M.G., Bessières P., Bolotin A., Borcher S.,
 RA Borriss R., Bourstler L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano N.V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings J., Daniel R.A.,
 RA Dentzof F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entlan K.D., Errington J., Fabret C., Ferrati E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golighly E.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Hensut A.,
 RA Hilbert H., Holstappel S., Hosono S., Hullo M.F., Iaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klier-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel N.C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Mestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogasawa K., Ogihara A., Oudeg B., Park S.H.,
 RA Pario V., Pohl T.M., Portetalle D., Porroport G., Ray M., Reynolds S.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Ray M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Schreier R., Scoffone F.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Taccori E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tononi A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vamler F., Vasseroiti A.,
 RA Viari A., Wambolt R., Wedler E., Wedler H., Wetzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Darchan A.,
 RT "the complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*."
 RT Nature 390:249-256(1997).
 RL -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>;
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL: X73124; CAAS1638.1; -
 DR EMBL: 299123; CAB15799.1; -
 DR PIR: S39737; S39737.
 DR HSSP: P50162; IAE1.
 DR Subtilast: RG10628; ywfd.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 KM Hypothetical protein; Oxidoreductase; Complete proteome.
 FT NP_BIND 11 33 NAD OR NADP (BY SIMILARITY).
 FT ACT_SITE 154 154 BY SIMILARITY.
 SQ SEQUENCE 255 AA; 27324 MW; 20AA225BFB869B CRC64;

Query Match 23.1%; Score 301; DB 1; Length 255;
 Best Local Similarity 32.7%; Pred. No. 5,6e-16;
 Matches 88; Conservative 42; Mismatches 93; Indels 46; Gaps 8;

QY 14 VTGGASGGLTAERLVGAGASAVLLDLPNSGGEQAOKLGNVVFAPADYTSKDQ 72
 DB 11 LTGGASGIGYAVVQAFLEQAVVAVADIDEAGGAVKRENDRLHEVQDTIDDAQC 70
 QY 73 TALALAKGKRGYDVAVNCAGIYVASKTYNLKKGQTHTEDFORVLDVNLMTGFNIR 130
 DB 71 HAYBSAVHTFGDLVILNNGIETIVAPIHEME-----LSDMKVLYQVNLGTGFLSKNA 124
 QY 131 -----LVAGEGQNEPDGQGGVYINTASVAAEFGVGAAYASASAGGIVGMLPIARDL 186
 DB 125 LKHLTAAG-----KGNINTCVSGIYVAMPDIPATYNAKSGVGLQTLTKSAVADY 172

QY 187 APGIRWMTAPGLFEGPLLTSLPEKVCNLF-----ASGVPPPSLGDPAEY 233
 DB 173 AKHGIYVNCVCGPIIDP-----LNKE--SFLENNGTLEIRKREKAKVNLRLRGPEEL 226
 QY 234 AHVQAITE--NPLNGEVIRLDGAIMQ 260
 DB 227 ANVMLFASDLSTWTSATADGCTTAQ 255

RESULT 16
 2BHD_STREX
 ID 2BHD_STREX STANDARD: PRT: 255 AA.
 AC P19992
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1991 (Rel. 35, Last annotation update)
 DE 20-beta-hydroxysteroid dehydrogenase (EC 1.1.1.53).
 OS Streptomyces exfoliatus (Streptomyces hydroganus).
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Streptomyces; Streptomyces; Streptomyces.
 CX NCBI_TaxID=1903;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90306362; PubMed=2194840;
 RA Marekov L., Krook M., Joernvall H.;
 RT "Prokaryotic 20 beta-hydroxysteroid dehydrogenase is an enzyme of the
 RT 'short-chain, non-metalloenzyme' alcohol dehydrogenase type."
 RL FEBS Lett. 266:51-54(1990).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=92052211; PubMed=1946424;
 RA Ghosh D., Weeks C.M., Grochulski P., Duax W.L., Erman M.,
 RA Rimsay R.L., Orr J.C.;
 RT "Three-dimensional structure of holo 3 alpha,20 beta-hydroxysteroid
 RT dehydrogenase: a member of a short-chain dehydrogenase family."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:10064-10068(1991).
 CC -1- CATALYTIC ACTIVITY: Androstane-3-alpha,17-beta-diol + NAD(+) = 17-
 CC beta-hydroxyandrostane-3-one + NADH.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 DR PIR: S10707; S10707.
 DR PDB: ZHD; 31-AUG-94.
 DR PDB: 1HDC; 07-FEB-95.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 KM Oxidoreductase; NAD; Steroid metabolism; 3D-structure.
 FT NP_BIND 10 34 NAD (BY SIMILARITY).
 FT ACT_SITE 152 152
 SQ SEQUENCE 255 AA; 26484 MW; 9CB93CB66AA628D5 CRC64;

Query Match 22.9%; Score 299; DB 1; Length 255;
 Best Local Similarity 33.6%; Pred. No. 7,9e-16;
 Matches 85; Conservative 47; Mismatches 101; Indels 20; Gaps 8;

QY 8 VGLVAVITGASGGLTAERLVGAGASAVLLDLPNSGGEQAOKLGNVVFAPADYTS 67
 DB 4 LSGKTVIITIGARGGAEARQAVAGARVYLDVDEGATARELDPAARYOHTDVTI 63
 QY 68 EKDVOYATLALAKGKRGYDVAVNCAGIYVASKTYNLKKGQTHTEDFORVLDVNLMTGFN 127
 DB 64 EEDMORVVAAYAEESGSDGLVNNAGISTGFL-----EIESVRFKRYVDINTLGVFI 117
 QY 128 VTRLVAGEGQNEPDGQGGVYINTASVAAEFGVGAAYASASAGGIVGMLPIARDLA 187
 DB 118 GKRTIYPAV---KDAAG--GSIVNISAAGIMGIALTSSGASGKVGSLKLAAYELG 171
 QY 188 PGIIVYMTAPGLFEGPL--TSLEPKVCNLFASVPPPSRLG--DPAEYALVQAITE-- 242
 DB 172 TDRIRVNSVHPQMTYPTAETGIRQGGNT--PNTPR--GRVGNBPGELIAGAVVKKLSDT 228

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL: U34072; AAC53573.1; -
 DR EMBL: U34072; AAC53574.1; -
 DR EMBL: AF100956; AAC69902.1; -
 DR HSSP: 070351; 186M.
 DR MGD: MGI:95911; H2-Re6.
 DR InterPro: IPR002198; ADH-short.
 DR Pfam: PF00106; adh_short; 1.
 DR PROSITE: PS00061; ADH.SHORT; 1.
 DR Steroid biosynthesis; Oxidoreductase; NAD; Multigene family;
 KM Alternative splicing.
 FT NP_BIND 13 38 NAD (BY SIMILARITY).
 FT ACT_SITE 168 168 BY SIMILARITY.
 FT VARSPLIC 257 260 GLEM -> MRSWGGGCGENTQVYMRK (IN LONG
 FT ISOFORM) G->GSVPSQ (IN REF. 3).
 FT CONFLICT 16 16 MISSING (IN REF. 1).
 FT CONFLICT 17 17 E -> EG (IN REF. 1).
 FT CONFLICT 230 230 E -> EG (IN REF. 1).
 SQ SEQUENCE 260 AA; 26645 MW; 19C712FCDD168B08 CRC64;

Query Match 24.0%; Score 313.5; DB 1; Length 260;
 Best Local Similarity 31.0%; Pred. No. 6.4e-17;
 Matches 85; Conservative 54; Mismatches 106; Indels 29; Gaps 9;

QY 1 MAACRSYKGLVAVITGCA-SGLGLAFAERLVGGASAVLLDPSNGSGEQAARKIGN-- 56
 DB 1 MASQLR-LRSALALVYTGAGSGAGSIRATSVRLAAGAAVAACDDGAAADQTVRLGSPGS 59
 QY 57 -----NVYFAPADYTSERDVOGTALALAKGKGR--VDVAVNAGIAVASKITNKKQ 107
 DB 60 EDGAPRGHAAAF-QADVSQGPAPARRLLEVOACSRPPSVVSCAGITRDEFLHMSF-- 116
 QY 108 THLEDFQRLVDVNLMTGFNVIRLVAGEMGNEPDGQGRGVINTASVAAFEGOVQAA 167
 DB 117 ----EDMDRVIAVNLKGTFLVYTAQAALVSS-----GGROSINISIIIGKVNIGQTN 167
 QY 168 YSASKGIVGKLTLLIARDLAPIGIRVFIAGLFGTLLLSLPKVCNFIASQVPPFSRL 227
 DB 168 YASSNAGVIGLQTPAARLGRHGRCSNVLPGFATPTOMPKVADKVTAMIP-L-GHM 226
 QY 228 GDPAEVYAHLYQ--AIENPFLNGEVIRLDGAIIR 259
 DB 227 GDPEDVADVVAFLASEDSGVTGASVEVSGGLFM 260

RESULT 13
 FABG_BACSU STANDARD; PRT; 246 AA.
 ID FABG_BACSU
 AC P51831; G31733;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
 DE acyl carrier protein reductase).
 GN FABG.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA MEDLINE=96326321; PubMed=8759840;
 RA Mordidont H.R., de Mendoza D., Cronan J.E. Jr.,
 RT "Bacillus subtilis acyl carrier protein is encoded in a cluster of
 RT lipid biosynthesis genes";
 RL J. Bacteriol. 178:4794-4800(1996).
 KW

RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Aevedo V., Bertorello M.G., Bessieres P., Bolotin A., Borcherdt S.,
 RA Bortiss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusler C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Ertlin K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guilseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holstappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Kjaer-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogikawa A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Potwilk S., Prescott A.M.,
 RA Pressean E., Puig P., Purnelle B., Rapoport G., Ray M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Serot S.J., Serot P., Shin B.S., Soldo B.,
 RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Takemoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vanlier F., Vassart A.,
 RA Viall A., Wambuit R., Wedler E., Wedler H., Welzenegger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yatsunoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis";
 RL Nature 380:249-256(1997).
 RN [3]
 RP SEQUENCE OF 1-172 FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98195738; PubMed=9534248;
 RA Foulger D., Errington J.;
 RT "A 28 kbp segment from the spore region of the Bacillus subtilis 168
 RT genome";
 RL Microbiology 144:801-805(1998).
 RN [4]
 RP SEQUENCE OF 230-246 FROM N.A.
 RC STRAIN=168;
 RA Oguero A., Kakeshita H., Takamatsu H., Nakamura K., Yamane K.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) -> 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL: U59433; CAB44307.1; -
 DR EMBL: 298112; CAB13466.1; -
 DR EMBL: Y13937; CAB4250.1; -
 DR EMBL: D64116; BAA10974.1; -
 DR HSSP: Q12634; 1YBV.
 DR Subtilist: Bg11535; fabG.
 DR InterPro: IPR002198; ADH-short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH.SHORT; FALSE_NEG.
 KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.


```

D6  NPESIAVAKAITDEGGVDILVNNAGITROBLMRKE-----EEMSDIMENLUSIF 115
QY  127 NVRRLVAGEMGNEPQQGRCGVYINTASVAAFEGVQCAAYSASKSGIVGMYLPARDL 166
D6  116 RLSRAVLGRMMK-----RGRRIIVGSGVGTGMAQCAVYAAKAGVIEFTSKMREV 169
QY  187 APIGRIVMTIAPILFEGTPLLSTLPEKVCNFTLSQVFFPSRJDPAEVAHVLQAIIEP-- 244
D6  170 ASHGVIYNNVAPBEFIETDWTKALNDEQRATLACVP-AGRGDPREIASAV-ATLASPEA 227
QY  245 -FLNGEYIRLDGAIRM 259
D6  228 AYTGTGELHAVNGMYM 243

```

RESULT	11
FAGL_SYNY3	
ID	FAGL_SYNY3
AC	P73574
DT	15-DEC-1998 (Rel. 37, Created)
DT	15-DEC-1998 (Rel. 37, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	3-oxoacyl-[acyl-carrier protein] reductase 1 (EC 1.1.1.100) (3-oxoacyl-acyl carrier protein reductase 1).
DE	FAGL1 OR SLR0886.
GN	Synechocystis sp. (strain PCC 6803) ;
OS	Synechocystis 86.
OC	Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
XC	NCBI_taxid=1148;

RX MEDLINE=97061201; PubMed=8905231;
 RA Kameo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirosewa M., Suglura M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Natsu K., Okumura S
 RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yanada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -1. CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1. PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1. SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on the use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/sib.ch>) or send an email to license@sib-sib.ch.

CC -----
DR EMBL, D90907; BAAL7614.1; .
DR HSSP; P50162; 1AE1.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short: 1.
DR PRINTS; PR00080; SDRPFAMLY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KM Fatty acid biosynthesis1; Oxidoreductase; NADP; Complete proteome.
FT NP_BIND 11 35 NADP (BY SIMILARITY).
FT ACT_SITE 156 156 BY SIMILARITY.
SQ SEQUENCE 247 AA; 25724 MW; 91EBF9409C77FF20 CRC64;

Query Match	24.0%	Score 313.5	DB 1	Length 247
Best Local Similarity	32.1%	Pred. No. 6.1e-17		
Matches 85	Conservative 45	Mismatches 92	Indels 43	Gaps 8

QY 12 VAVITGASIGLATAERLVCG-----ASAVIDLPNSGGEAQAKKLGNNV 58
||::|| : ||| ||| | | ||| :: : ||||

```

Db      8 VALVTGASRIGKATLALAAATGMKVVVYAQSSPAADAAYAAEIIANGGEA----- 58

Qy      59 VEPADVTSEKDYQTLLALAKRGFGVYVAANCALIAVASTYNUKKGQHTTLEDPQRYL 118
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      59 IAVQAVYANNADEVDOLIKTTLDKFSFIDVLVNNAGITBDTLLRRK-----LEDQAVI 112

Qy      119 DVNLMTGFNNIRLVAGEMCONEPDGGQGRVYINFTASVAAEFGQVQALYASASKGJIVGM 178
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      113 DLNLTGVEFLCTKRAVSKLMLKQ-----KSGRIINITSVAGMKNPGQANYSAAAGYIGF 166

Qy      179 TLEPIARDLAPIGIRVMTIAPGLEFGPPLTSL-PEVVCNFLASQVFPBSRLGDPREYVHLV 237
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      167 TKTVAKELASRGVTVANVAPGFATMDMENTLNAEPILOF---IPL-ARYQCPREYVAGTI 221
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      238 QAIIEFP---FLNGEYIRLDGAIRM 259

Db      222 RFLATDPAAYITGQTFNNVDGGKVM 246
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

ID	DB8_MOUSE	STANDARD:	PRT:	260 AA.
AC	P50171;	Q60959;	Q60958;	Q921W2;
DT	01-OCT-1996	(Rel. 34,	Created)	
DT	01-OCT-1996	(Rel. 34,	Last sequence update)	
DT	16-OCT-2001	(Rel. 40,	Last annotation update)	
DE	Estradiol 17 beta-dehydrogenase 8 (EC 1.1.1.62) (17-beta-HSD 8) (17-			
DE	beta-hydroxysteroid dehydrogenase 8) (K6b protein) (K6-)			
GN	HS17B8 OR HKE6 OR H2-K6D.			

OS Mus musculus (Mouse).
OC Eukaryota; Neozoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN
RN (1)
RP SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RC MEDLINE=93180832; PubMed=8441417;
RX Aziz N., Maxwell M.M., St Jacques B., Brenner B.M.;
RA "Downregulation of Ke 6, a novel gene encoded within the major
RT histocompatibility complex, in murine polycystic kidney disease."
RL Mo. Cell. Biol. 13:1847-1853(1993).

RN [2]
 RP ERRATUM.
 RA Aziz N., Maxwell M.M., St Jacques B., Brenner B.M.;
 RL Mol. Cell. Biol. 13:6614-6614 (1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=96027630; Pubmed=7559658;
 RA Maxwell M.M., Nearing J., Aziz N.;
 RT "K6 gene. Sequence and organization and aberrant regulation in
 RL murine polycystic kidney disease." J. Biol. Chem. 270:25213-25219 (1995).

RN [4] SEQUENCE FROM N.A.
 RP STRAIN-129/SVJ.
 RC Roven L., Qin S., Madan A., Loretz C., James R., Dors M., Mix L.,
 RA Hall J., Iasky S., Hood L.,
 RA "Sequence of the mouse major histocompatibility locus II
 RT region."
 RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RI -1- FUNCTION: USES ESTRADIOL AS ITS PREFERRED SUBSTRATE.
 CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P)⁺ = estrone +
 CC NAD(P)H.
 CC -1- PATHWAY: BIOSYNTHESIS OF ESTROGENS.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A SHORT FORM (SHOWN HERE) AND

CC -1- TISSUE SPECIFICITY: KIDNEY, LIVER AND MODERATELY IN SPLEEN, HEART
CC AND BRAIN.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

CC (SUN) FAMILI :
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC -----

AC 092506; 09DI01;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Estradiol 17 beta-dehydrogenase 8 (EC 1.1.1.62) (17-beta-HSD 8) (17-
 DE beta-hydroxysteroid dehydrogenase 8) (Ke6 protein) (ke-6).
 GN HSD17B8 OR HK6 OR RING2 OR FABGL
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Tubbey B.;
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 3-261 FROM N.A.
 RX MEDLINE=97001166; PubMed=8812499;
 RA Ando A., Kikuchi Y., Shigenari A., Kawata H., Okamoto N., Shina T.,
 RA Chen L., Ikemura T., Abe K., Kimura M., Inoko H.;
 RT "cDNA cloning of the human homologues of the mouse Ke4 and Ke6 genes
 RT at the centromeric end of the human MHC region.";
 RL Genomics 35:600-602(1996).
 CC -1- FUNCTION: USES ESTRADIOL AS ITS PREFERRED SUBSTRATE.
 CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P)(+) = estrone +
 CC NAD(P)H.
 CC -1- PATHWAY: BIOSYNTHESIS OF ESTROGENS.
 CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE LIVER AND PANCREAS,
 CC LOWER IN THE SKELETAL MUSCLE AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SCR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AL031228; CAC38444.1;
 DR EMBL: D82061; BA11529.1;
 DR HSSP: 070351; 1B6W.
 DR GeneW: HGNC:3554; HSD17B8.
 DR MIM: 601417;
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 KW Steroid biosynthesis; Oxidoreductase; NAD; Multigene family.
 FT NP_BIND 15 39 NAD (BY SIMILARITY).
 FT ACT_SITE 169 169 E -> R (IN REF. 2).
 FT CONFLICT 117 117 R -> P (IN REF. 2).
 FT CONFLICT 193 193 R -> P (IN REF. 2).
 FT CONFLICT 208 208 Q -> K (IN REF. 2).
 FT CONFLICT 212 212 Q -> K (IN REF. 2).
 SQ SEQUENCE 261 AA; 26974 MW; 8B8B2D7131714D71 CRC64;
 Query Match 25.5%; Score 332.5; DB 1; Length 261;
 Best Local Similarity 31.2%; Pred. No. 2,4e-18;
 Matches 83; Conservative 51; Mismatches 103; Indels 27; Gaps 7;
 QY 8 VKGLAVITGASGLGATAEELVGGASAVLIDLPSNGGEQAQAKL-----GN 56
 DB 9 LRSALAVITGAGSGIGRAVSRYLAGEGATVAACDLDRAAQETVRLTGPGSKGPPRGN 68
 OY NVVAPADVTSEKVVQVQALAKGKGR-VDVAVNCAGIAVASTYLNKKGQTHLEDFQ 115
 DB 69 HAAE-QADVSEARARCLIEGVQNGFSRPPSVVSCAGITQDEFLHMS-----DDWD 121
 OY 116 RVLVDNLTGFTNTRIVAGENGONPDGQGVYINTASVAAEFGVQGAASAKGI 175
 DB 122 KVIAVNLKGFELVYQAQAALVSN-----GGRGSIINISSIVGKVGAVGQTNVAASRAGV 176

QY 176 VGMTLPARDLADIGIRVMTIAPGLFTPLTSLPERVCNFLASQVFPFSRLDGPAAEYAH 235
 DB 177 IGLTQFARLGRHGRINCNSVLPFGFIATPMTCVQKVDKITEMIPM-GHLDGDPDVAD 235
 OY 236 LVO-AATPEPFLNGEYIRLDGAIRM 259
 DB 236 VAFVASEDSGVTITGSVEYTGGLFM 261
 RESULT 10
 ID FABG_VIBCH STANDARD; PRT; 244 AA.
 AC Q9K0F7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
 DE acyl carrier protein reductase).
 GN FABG OR VC2021.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=566;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Ginn M.L.,
 RA Dodson R.J., Hatt D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Emolaeva M.D., Vamathevan J., Bass S., Qin H., Richter J., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae.";
 RL Nature 406:477-483(2000).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NAD(P)(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AE004276; AAF95169.1; ALT_INT.
 DR HSSP: P19992; IHDC.
 DR TIGR: VC2021;
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 10 34 NADP (BY SIMILARITY).
 FT ACT_SITE 151 151 BY SIMILARITY.
 SQ SEQUENCE 244 AA; 25566 MW; 9FB2E8278DCC3CE CRC64;
 Query Match 25.2%; Score 328.5; DB 1; Length 244;
 Best Local Similarity 32.0%; Pred. No. 4,4e-18;
 Matches 82; Conservative 54; Mismatches 103; Indels 17; Gaps 5;
 QY 7 SVKGLAVITGASGLGATAEELVGGASAVLIDLPSNGGEQAQAKLGNVVFAPADVT 66
 DB 2 NIEGRVALVTGASRGIGKAIADLEERKAKVIGTATSEGAQAIDYLGDNKGAALANT 61
 OY 67 SENDVOTALALAKGKGRVDVAVNCAGIAVASKTYLNKKGQTHLEDFQVLDVNLKGT 126

RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 genome sequence of *Thermotoga maritima*.";
 RL Nature 399:323-329(1999).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: A6001811; AAD36790.1; -
 DR HSSP: P50162; 1AEL.
 DR TIGR: TM1724; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Fatty acid biosynthesis; Oxidoreductase; NADP: Complete proteome.
 FT NP_BIND 10 NADP (BY SIMILARITY).
 FT ACT_SITE 154 154 BY SIMILARITY.
 SQ SEQUENCE 246 AA; 26401 MW; 8C08504D28099142 CRC64;
 Query Match 26.5%; Score 346; DB 1; Length 246;
 Best Local Similarity 34.1%; Pred. No. 2.1e-19;
 Matches 87; Conservative 47; Mismatches 103; Indels 18; Gaps 5;

QY 8 VKGLAVITGASGLGATAEALVGGASAVLLDLPNSGSEA---QAKKIGNVAVAPAD 64
 DB 3 LEGVVCITGASIGATATLLFRQEGATVYAGDISKENIDSLYKEEGJPGVADPVLN 62
 QY 65 VTSKDVQOTALALAKGFRGVAVNCAGIYASVSKYTNLKGQTHLEDFQVLYDLNMG 124
 DB 63 VTDSDQLEKVEYKVVQYGRIDVLVNNAGITRDALLVYRKE-----EDWDVAVINVLKG 116
 QY 125 TFNVITRLVAGMGONEDPOGQGVITINTASVAFEGQVGOAAYASAKSGIVGMLPIAR 184
 DB 117 VFNTQWVVPYMIQ-----RNGSIYVSSVVGIVNPGQTNVASKAGVIGTKTWAK 170
 QY 185 DLADIGIRVMTIAGLGTPTPLTSLPEKVCNFIASQVFPFRLDPAEYALV--QAII 242
 DB 171 ELAGNINNVNVAAGFIETPTEKTLPEKARETALSRLPL-GRFGKPEVAVQVILFLASDE 229
 QY 243 NPLNGEYIRLDGAI 257
 DB 230 SSYVIGVYIGIDGL 244

RESULT 8
 PABG_CUPHA STANDARD; PRT; 320 AA.
 ID PABG_CUPHA
 AC P28643;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase, chloroplast precursor
 DE (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
 GN CLKR27.
 OS Cuphea lanceolata.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Myrtales; Lythraceae; Cuphea.
 OC NCBI_TaxID=3930;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9229104; PubMed=1376402;
 RA Klein B., Pawlowski K., Hoerlicke-Grandpierre C., Schnell J.,
 RA Toepfer R.,
 RT "Isolation and characterization of a cDNA from *Cuphea lanceolata*
 RT encoding a beta-ketoacyl-ACP reductase.";
 RL Mol. Gen. Genet. 233:122-128(1992).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC
 CC PLASTIDS.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X64566; CAA45866.1; -
 DR PIR: S19832; S19832.
 DR HSSP: P50162; 1AEL.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Fatty acid biosynthesis; Oxidoreductase; NADP; Chloroplast;
 KW Transit peptide.
 FT TRANSIT 1 61 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 61 3-oxoacyl-[acyl-carrier protein]
 FT NP_BIND 82 106 REDUCTASE.
 FT ACT_SITE 227 227 NADP (BY SIMILARITY).
 SQ SEQUENCE 320 AA; 33103 MW; 06BAF0522B28C87 CRC64;
 Query Match 25.6%; Score 334; DB 1; Length 320;
 Best Local Similarity 32.7%; Pred. No. 2.3e-18;
 Matches 87; Conservative 46; Mismatches 111; Indels 22; Gaps 6;

QY 2 AAGRSVKGIVAVITGASGLGATAEALVGGASAVLLDLPNSGSEA---QAKKIGN 56
 DB 69 AGAGSVESPVYIVICASGIDKALALSL-GRAGKVLNVAVRSSKEAEVSKIEARGG 127
 QY 57 NVFADADYTSKDVOTALALAKGFRGVAVNCAGIYASVSKYTNLKGQTHLEDFQV 116
 DB 128 QALTFGDVSKEDVEMIKITAVDANGIVDILVNNAGITRDGLIMRKISQ-----WQE 181
 QY 117 VLDVNLGTFNVNTRIVAGMGONEDPOGQGVITINTASVAFEGQVGOAAYASAKSGIV 176
 DB 182 VIDNLNLTGFLCQAAKIMKK-----KKGIINIASVVGIVYAGNAGANSAKAGVI 235
 QY 177 GMTLPARDIAPIGIRVMTIAGLGTPTPLTSLPEKVCNFIASQVFPFRLDPAEYALV 236
 DB 236 GFTKVAAREYASRNINNVAVAPFISDWTSKLDGIDINKKIETIPL-GRYQPEVAVGL 294
 QY 237 VOALINP---FLNGEYIRLDGAI 259
 DB 295 VERFLAINPASSYVIGVYITDGMT 320

RESULT 9
 DH88_HUMAN STANDARD; PRT; 261 AA.
 ID DH88_HUMAN

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA;
 RA Fu J., Chen X., Stern D., Yan S.D.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
 CC + NADH.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U96116; AAB57689.1; ALT_INT.
 DR HSSP: O70351; 186M.
 DR SWISS-2DPAGE: O08756; MOUSE.
 DR MGI: MGI:133871; Hsd17b10.
 DR InterPro: IPR002198; ADH_Short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Oxidoreductase; NAD.
 KW NP_BIND 12 NAD (BY SIMILARITY).
 FT ACT_SITE 168 168 BY SIMILARITY.
 FT SEQUENCE 261 AA; 27418 MW; 6121381352839D41 CRC64;
 SQ
 Query Match
 Best Local Similarity 85.0%; Score 1122; DB 1; Length 261;
 Matches 224; Conservative 19; Mismatches 18; Indels 0; Gaps 0;
 QY 1 MAACRSYKGLVAVITGASGLGATARLVGCGASAVILDLPSGGEAOAKKIGNVVF 60
 DB 1 MAARSVKGLVAVVTGGASGPMATARKLVGGATALLDVPSESGSOKKLGESCIF 60
 QY 61 APADVTSKDVQOTALALAKGKFGKRDVAVNAGIAVASKTYNKKGGTHLEDFQRLDV 120
 DB 61 APANTSKSEIQALALTLAKKEFGKRDVAVNAGIAVAKTKYHKKKTHLEDFQRYINV 120
 QY 121 NLMGFNVIRLVAGMGNGNEPDGQGRVITNTASVAFEEQVQCAAYSAKSGITVMTL 180
 DB 121 NLIGFNVIRLVAGMGNGNEPDGQGRVITNTASVAFEEQVQCAAYSAKSGITVMTL 180
 QY 181 PIARDIAPIGIRVMITAPLGTPLTSLPEKVCNFTLASQVFPFSRLDPAEVAHLVQAI 240
 DB 181 PIARDIAPIGIRVMITAPLGTPLTSLPEKVCNFTLASQVFPFSRLDPAEVAHLVQAI 240
 QY 241 IENPLNGEVIRLDGAIKQIP 261
 DB 241 IENPLNGEVIRLDGAIKQIP 261
 RESULT 5
 HCD2_DROME STANDARD: PRT: 255 AA.
 ID HCD2_DROME
 AC 018404;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)
 DE (Scully protein).
 GN SCU OR CG7113.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LEU-33 AND PHE-120.
 RC STRAIN=canon-S;
 RA MEDLINE=98252852; PubMed=9585418;
 RT Torroja L., Ortuno-Sabaun D., Ferrus A., Haemmerle B., Barbas J.A.;
 RT Scully, an essential gene of Drosophila, is homologous to mammalian
 RT mitochondrial type II L-3-hydroxyacyl-CoA dehydrogenase/amyloid-beta
 RT peptide-binding protein.
 RT J. Cell Biol. 141:1009-1016(1998).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Berkeley;
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.C., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.H.C., Blazer R.G., Chapple M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
 RA Ballwe R.M., Basu A., Bakendale J., Bayraktaroglu U., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Moberly C., Morris J., Moshirefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Schaefer F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson W., Skupski M.P., Smith T.,
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Stryker R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 CC Science 287:2185-2195(2000).
 CC -1- FUNCTION: MAY PLAY A ROLE IN GERM LINE FORMATION.
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
 CC + NADH.
 CC -1- SUBUNIT: MULTIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
 CC -1- TISSUE SPECIFICITY: FOUND IN MANY TISSUES INCLUDING CNS. HIGHEST
 CC EXPRESSION IN BOTH EMBRYONIC GONADAL PRIMORDIA AND MATURE OVARIES
 CC AND TESTES.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

entitles requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; AB002156; BAA19510.1; -

DR HSSP; O70351; 1E6W.

DR InterPro; IPR002198; ADH_short.

DR Pfam; PF00106; adh_short; 1.

DR PRINTS; PRO0080; SDRFAMILY.

DR PROSITE; PS00061; ADH_SHORT; 1.

KM Oxidoreductase; NAD; Mitochondrion.

FT NP_BIND 12 NAD (By SIMILARITY).

FT ACT_SITE 168 168 BY SIMILARITY.

SQ SEQUENCE 261 AA; 27140 MM; 8C7572B6A9A9780 CRC64;

Query Match 91.7%; Score 1196; DB 1; Length 261;

Best Local Similarity 91.6%; Pred. No. 1.2e-83;

Matches 239; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGGASGLGATARLVGGASAVLLDPSNGGEPAQKKGNNVF 60

DB 1 MAACRSYKGLVAVITGGASGLGATARLVGGASAVLLDPSNGGEPAQKKGSCAF 60

QY 61 APADYTSKDYQOTALALAKGKFGRYDAVANCAGIAVASKTYNLKKGQHTLEDFQRLDV 120

DB 61 APADYTSKDYQOTALALAKGKFGRYDAVANCAGIAVASKTYNLKKQAHTLEDFQRLDV 120

QY 121 NLMGTFNIRLVAGEMGNEDDGGQRCVITNTASVAEFEGVQQAAYSAKSGIVGML 180

DB 121 NLGTFNIRLVAGEMGNEDDGGQRCVITNTASVAEFEGVQQAAYSAKSGIVGML 180

QY 181 PLARDLPIGIRVMTIAPGLFGTPLTSLPERKCNFLASQVPPFSRLGDPAPVYAHVLQVAI 240

DB 181 PLARDLPIGIRVMTIAPGLFGTPLTSLPERKCNFLASQVPPFSRLGDPAPVYAHVLQVAI 240

QY 241 ENPFLNGEVIRLDGAIKMQP 261

DB 241 ENPFLNGEVIRLDGAIKMQP 261

RESULT 3

HCD2_RAT STANDARD; PRT; 260 AA.

AC 070351; Q9GYD4; (Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)

DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein).

GN HADH2 OR ERAB.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Gunn-Moore F.J., Tavaré J.M.;

RT "Rattus norvegicus amyloid beta-peptide binding protein (ERAB) mRNA.";

RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.

RN (2)

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;

RA Yang S.-Y., He X.-Y.;

RT "Molecular cloning and characterization of the cDNA of rat brain short chain L-3-hydroxyacyl-CoA dehydrogenase.";

RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.

RN (3)

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RC TISSUE=Brain;

RA MEDLINE=20481418; PubMed=11023795; Powell A.J., Read J.A., Banfield M.J., Gunn-Moore F., Yan S.D.,

RT "Recognition of structurally diverse substrates by type II

RT 3-hydroxyacyl-CoA dehydrogenase (HADH II)/amyloid-beta binding

RT alcohol dehydrogenase (ABAD).";

RL J. Mol. Biol. 303:311-327(2000).

CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.

CC -1- SUBUNIT: HOMOTETRAMER.

CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; AF049878; AAC05747.1; -

DR EMBL; AF069770; AAF14653.1; -

DR PDB; 1E3W; 25-MAY-01.

DR PDB; 1E3S; 25-MAY-01.

DR PDB; 1E6W; 25-MAY-01.

DR InterPro; IPR002198; ADH_short.

DR Pfam; PF00106; adh_short; 1.

DR PRINTS; PRO0080; SDRFAMILY.

DR PROSITE; PS00061; ADH_SHORT; 1.

KM Oxidoreductase; NAD; Acetylation; 3D-structure.

FT INIT_MET 0 BY SIMILARITY.

FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).

FT NP_BIND 11 36 NAD (BY SIMILARITY).

FT ACT_SITE 167 167 BY SIMILARITY.

FT CONFLICT 4 4 V -> C (IN REF. 2).

SQ SEQUENCE 260 AA; 27114 MM; 30F7E72A95F9227 CRC64;

Query Match 87.5%; Score 1141; DB 1; Length 260;

Best Local Similarity 87.3%; Pred. No. 1.7e-79;

Matches 227; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 2 AAACRSYKGLVAVITGGASGLGATARLVGGASAVLLDPSNGGEPAQKKGNNVFA 61

DB 1 AAACRSYKGLVAVITGGASGLGATARLVGGASAVLLDPSNGGEPAQKKGNNVFA 60

QY 62 PADYTSKDYQOTALALAKGKFGRYDAVANCAGIAVASKTYNLKKGQHTLEDFQRLDV 121

DB 61 PANTSEKDYQOTALALAKGKFGRYDAVANCAGIAVASKTYNLKKGQHTLEDFQRLDV 120

QY 122 LMGTFNIRLVAGEMGNEDDGGQRCVITNTASVAEFEGVQQAAYSAKSGIVGML 181

DB 122 LMGTFNIRLVAGEMGNEDDGGQRCVITNTASVAEFEGVQQAAYSAKSGIVGML 180

QY 181 PLARDLPIGIRVMTIAPGLFGTPLTSLPERKCNFLASQVPPFSRLGDPAPVYAHVLQVAI 241

DB 181 PLARDLPIGIRVMTIAPGLFGTPLTSLPERKCNFLASQVPPFSRLGDPAPVYAHVLQVAI 240

QY 242 ENPFLNGEVIRLDGAIKMQP 261

DB 241 ENPFLNGEVIRLDGAIKMQP 260

RESULT 4

HCD2_MOUSE STANDARD; PRT; 261 AA.

AC 008756;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)

DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein).

GN HADH2 OR HSD17B10 OR ERAB.

HCDD2_HUMAN STANDARD; PRT; 261 AA.
 ID HCDD2_HUMAN
 AC Q99714;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)
 DE (Endoplasmic reticulum-associated amyloid beta-peptide binding
 protein) (Short-chain type dehydrogenase/reductase XH96G2).
 GN HADH2 OR ERAB OR XH96G2 OR SCHAD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RX MEDLINE=97478528; PubMed=9338779;
 RA Yan S.D., Fu J., Soto C., Chen X., Zhu H., Al-Mohanna F.,
 RA Collinson K., Zhu A., Stern E., Saldo T., Tohyama M., Ogawa S.,
 RA Rober A., Stern D.;
 RA "An intracellular protein that binds amyloid-beta peptide and
 RA mediates neurotoxicity in Alzheimer's disease.";
 RA Nature 389:689-695(1997).
 RN [2]
 RN SEQUENCE FROM N.A.
 RN Zhubchenko O.P., Wehnert M., Bailey J., Sun Z.S., Lee C.C.;
 RN Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RN MEDLINE=98337980; PubMed=9671743;
 RA Miller A.P., Willard H.F.;
 RA "Chromosomal basis of X chromosome inactivation: Identification of a
 RA multigene domain in Xp11.21-p11.22 that escapes X inactivation.";
 RA Proc. Natl. Acad. Sci. U.S.A. 95:8709-8714(1998).
 RN [4]
 RN SEQUENCE FROM N.A.
 RN TISSUE=Brain;
 RX MEDLINE=96221216; PubMed=9553139;
 RA He X.Y., Schulz H., Yang S.Y.;
 RA "A human brain L-3-hydroxyacyl-coenzyme A dehydrogenase is identical
 RA to an amyloid beta-peptide-binding protein involved in Alzheimer's
 RA disease.";
 RA J. Biol. Chem. 273:10741-10746(1998).
 RN [5]
 RN SEQUENCE FROM N.A.
 RN TISSUE=Lung;
 RA Strausberg R.;
 RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: BINDS INTRACELLULAR AMYLOID-BETA. BY INTERACTING WITH
 CC AMYLOID-BETA, IT MAY CONTRIBUTE TO THE NEURONAL DYSFUNCTION
 CC ASSOCIATED WITH ALZHEIMER DISEASE.
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
 CC + NADH.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN NORMAL TISSUES BUT IS
 CC OVEREXPRESSED IN NEURONS AFFECTED IN AD.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SCR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL, U96132; AAC51812.1; -
 CC EMBL, U73514; AAB68958.1; -
 CC EMBL, AF069134; AAC39900.1; -
 CC EMBL, AF035555; AAC15902.1; -
 CC EMBL, AF037438; AAC16419.1; -

DR EMBL, BC000372; AAH00372.1; -
 DR HSSP; O70351; 1E3S.
 DR Genew; HGNC:4800; HADH2.
 DR MIM; 300256; -
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KW Oxidoreductase, NAD.
 FT NP_BIND 12 37 NAD (BY SIMILARITY).
 FT ACT_SITE 168 168 BY SIMILARITY.
 FT ACT_SITE 168 168
 SQ SEQUENCE 261 AA; 26923 MW; 9E74F242E3E6FEF1 CRC64;
 Query Match 99.6%; Score 1299; DA 1; Length 261;
 Best Local Similarity 99.6%; Pred. No. 1.9e-91;
 Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAAQRVYKGLVAIVTGGASGIGLATPRLVGGASAVLLDIPNSGGEAQAQKGNVVF 60
 DB 1 MAAQRVYKGLVAIVTGGASGIGLATPRLVGGASAVLLDIPNSGGEAQAQKGNVVF 60
 QY 61 APADTSEEDVQFALALAKGKFRGVAVNCAGIVASKTYNLRKQTHTEDFQRLDV 120
 DB 61 APADTSEEDVQFALALAKGKFRGVAVNCAGIVASKTYNLRKQTHTEDFQRLDV 120
 QY 121 NMGTFFNTRLVAGENGQNEPDGQGVITNTASVAAPFGVGGAAVSASKGIVGWL 180
 DB 121 NMGTFFNTRLVAGENGQNEPDGQGVITNTASVAAPFGVGGAAVSASKGIVGWL 180
 QY 122 NMGTFFNTRLVAGENGQNEPDGQGVITNTASVAAPFGVGGAAVSASKGIVGWL 180
 DB 122 NMGTFFNTRLVAGENGQNEPDGQGVITNTASVAAPFGVGGAAVSASKGIVGWL 180
 QY 181 PIARDLAPIGIRVMTAPGLFGLTSLPERVCNFIASQVPEPSRLGPAPRYAHLVQAI 240
 DB 181 PIARDLAPIGIRVMTAPGLFGLTSLPERVCNFIASQVPEPSRLGPAPRYAHLVQAI 240
 QY 241 IENPFLNGEYIRLDGAIKMP 261
 DB 241 IENPFLNGEYIRLDGAIKMP 261
 QY 241 IENPFLNGEYIRLDGAIKMP 261
 DB 241 IENPFLNGEYIRLDGAIKMP 261
 RESULT 2
 HCDD2_BOVIN STANDARD; PRT; 261 AA.
 ID HCDD2_BOVIN
 AC 002691;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH).
 GN HADH2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NC NCBI_TaxID=9913;
 RX MEDLINE=97214648; PubMed=9061028;
 RA Furuta S., Kobayashi A., Miyazawa S., Hashimoto T.;
 RA "Cloning and expression of cDNA for a newly identified isozyme of
 RA bovine liver 3-hydroxyacyl-CoA dehydrogenase and its import into
 RA mitochondria.";
 RL Biochim. Biophys. Acta 1350:317-324(1997).
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
 CC + NADH.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SCR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial

DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase.
 GN FABG OR ALR1894.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 RT cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 RL EMBL; AP003587; BAB73593.1; -;
 DR InterPro; IPR002198; ADH_Short.
 DR InterPro; IPR001092; HLH_Basic.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 KM Complete proteome.
 SQ SEQUENCE 251 AA; 26218 MW; 57D0712FE8A6B698 CRC64;

Query Match 25.7%; Score 334.5; DB 16; Length 251;
 Best Local Similarity 33.1%; Pred. No. 2.6e-15;
 Matches 91; Conservative 46; Mismatches 97; Indels 41; Gaps 7;

QY	1	MAACRSYKGLVAVITGASGLIATARLYGQASA-----VLDLPNSGG	47
DB	1	MAIASENLRGQVAVVTGASRGIGRAIALELANYGATVYVYASSSTADEVVAELTGAGG	60
QY	48	EAOAKKLGNNVVFAPADVTSEKDVQFALALAKGKFRVDVAVNCAGIYAVASKTYNLKKGQ	107
DB	61	EAVALK-----ADVSQVEQVDNLNGAIDKFRIDILVNNAGITRDITLLRMKP--	109
QY	108	THLEDFQRLVDVNLMGTFENVIRLVAGEMGONEPDGQGRGVITNTASVAAFESQVQQA	167
DB	110	----EDMQAVIDLNTGVFLCTRAVSKMLKQ-----RSGRIITITSVAGOMGNPGQAN	159
QY	168	YSASKGIIVGWTLPFARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPSPRL	227
DB	160	YSAKAGYIGFTKYAKELASRGITVNVNAPGFATIDTSTLKSE---GIQYIPL-GRY	215
QY	228	GDPAEYAHVQAIIENP--FLNGEVIRLDGAIRM	259
DB	216	GQPEIAGVRFLLADPAAAYITGQVFNVGDMVM	250

Search completed: June 23, 2003, 14:32:45
 Job time : 32.667 secs

Query Match 26.1%; Score 340.5; DB 3; Length 297;
 Best Local Similarity 32.0%; Pred. No. 1.3e-15;
 Matches 98; Conservative 39; Mismatches 102; Indels 67; Gaps 8;

QY 6 RSVYGLVAVITGGASGLATAEFLVCGASAVILDPNS-----GGEAQ 50
 DB 2 RSLLEKQALITGGSGIGLAIARLRLLEGCSVTLTGTESTLQASQSLLSLPLSPAQ 61
 QY 51 AKRLGNVVFAPAVTSEKDVQTL-ALAKGFGRVAVANAGIAVAS--KTYNLKG 106
 DB 62 QPSDTKRSYHPLVNTASSMEDLLQNSNGKGRVDILNCGAIIIRSPLMKT----- 115
 QY 107 QTHLEDFORVLDVNLKGTENVIRLVAGENGQEP-----DQCG----- 145
 DB 116 ---SIEVEGILLDYNLRTYLGCKFVRAMLRNPSQOHPRVKADEGAGVEGTEEG 172
 QY 146 -----QRGVIINTASVAAFEGOVGAASASKGIVGKTLPIARDLAPIGI 191
 DB 173 KGEKGGQVRBGVQERGVITIVASLAKGVIGTSYNAAKAGVYGLITSLAHYGRSGI 232
 QY 192 RVMTIAPGLFSTPLTSLPERVCNPLASQVFPFSLDDPAEYAHVQATIEPFLNGEVI 251
 DB 233 RVNAVLPQYIETDMTGTGNP---SILQIPL-GRFGTDEVADALFLIKNPYANNCVL 288
 QY 252 RLDDGI 257
 DB 289 NLDGCL 294

RESULT 23
 Q8R9W0 PRELIMINARY; PRT; 247 AA.

AC 08R9W0
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Dehydrogenases with different specificities (related to short-chain
 DE alcohol dehydrogenases).
 GN FASG3 OR TTE1472.
 OS Thermoaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Thermoaerobacteriales; Thermoaerobacteriaceae; Thermoaerobacter.
 OC NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MBAT / JCM11007;
 RX MEDLINE=21992816; PubMed=11997336;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;
 RT "A complete sequence of T. tengcongensis genome.";
 RL Genome Res. 12:689-700(2002).
 DR EMBL; AE013105; AAM24694.1; -
 RN Complete proteome.
 SQ SEQUENCE 247 AA; 26606 MW; 357D82B8C60E7947 CRC64;

Query Match 25.9%; Score 337.5; DB 16; Length 247;
 Best Local Similarity 34.3%; Pred. No. 1.6e-15;
 Matches 87; Conservative 48; Mismatches 100; Indels 19; Gaps 6;

QY 12 VAVITGASGLIATAERLVCGASAVILDPN--SGGEA--QAKKLGNNVVFAPADYTS 67
 DB 7 VAVITGASGLIATAERLVCGASAVILDPN--SGGEA--QAKKLGNNVVFAPADYTS 67
 QY 68 EKDVTALALAKGFRGVAVVNCAGIYAVASKTYNLKKGQTHLEDFORVLDVNLKGTEN 127
 DB 67 YHEVEKAVERKYLEEGSIDVYVNNAGITKMLILKMEB-----EEMDQVLDVNLKGAFN 120
 QY 128 VIRLVAGMGONEPDGQGRGVIINTASVAAFEGOVGAASASKGIVGKTLPIARDLIA 187
 DB 121 VIKFSKTMKK-----KRGKIINISSVGLMGVNGVAGANPAASKAGITGITKSYAKELA 174
 QY 188 PIGIRVMTIAPGLFSTPLTSLPERVCNPLASQVFPFSLDDPAEYAHVQ--AIENPF 245

DB 175 SRGITVNAVAPGITEIDMTNVLKEDIKEMLKSIPL-KRAGRPDEVAEYVAFIASSASDY 233
 QY 246 LINGEVRIDGAIYM 259
 DB 234 ITGQVIVNDGKVM 247

RESULT 24
 Q9K636 PRELIMINARY; PRT; 246 AA.

AC 09K636
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 3-oxoacyl-(acyl-carrier protein) reductase.
 GN BH3896.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OC NCBI_TaxID=66655;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC EMBL; AP001520; BAB07615.1; -
 DR HSSP; P19992; IHDC.
 DR InterPro; IPR002196; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
 KM Oxidoreductase; Complete proteome.
 SQ SEQUENCE 246 AA; 26357 MW; 7CEAB2C4E155376 CRC64;

Query Match 25.7%; Score 335; DB 16; Length 246;
 Best Local Similarity 34.6%; Pred. No. 2.4e-15;
 Matches 92; Conservative 40; Mismatches 94; Indels 40; Gaps 8;

QY 8 VKGVAVITGASGLIATAERLVCGASAVILDPN-----LPNSGGEPAQAKRTG 55
 DB 3 LNKGVAMITGAGGIGATKAKKFAREGAKYIVCDVAEEYAKTYVAIIOGGGA-----LG 58
 QY 56 NNVVFAPADYTSKDVQTLALAKGFRGVAVVNCAGIYAVASKTYNLKKGQTHLEDFQ 115
 DB 59 SVV-----DVTQRKDYKVNINQVIERFETLDVYVNNAGITADQLTNMTDAQ-----WD 107
 QY 116 RVLDVNLKGTENVIRLVAGENGQEPDQGRGVIINTASVAAFEGOVGAASASKGIGI 175
 DB 108 DVIDVNLKGVITYTOEYTTMKEQ-----KRGVIINASSVVSYGFQGTINAAKMGV 161
 QY 176 VGNLPIARDLAPIGIRVMTIAPGLFSTPLTSLPERVCNPLASQVFPFSLDDPAE--- 232
 DB 162 NGMTKTAKELGRVIRVNAVAPGILITPTKMPKPVLYKMBEKAVL--NRLGTVEEVAN 220
 QY 233 -YAHVQATIEPFLNGEVRIDGAI 257
 DB 221 GYAFV--ASDEASPTGTITLIDGV 244

RESULT 25
 Q8YVTO PRELIMINARY; PRT; 251 AA.

AC 08YVTO
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Gardner R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
Brodly L.A., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.,
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
CC EMBL; AF004854; AAC07777.1; -
DR HSSP; P50163; 2AE1.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR OXIDOREDUCTASE; Complete proteome.
KW OXIDOREDUCTASE; Complete proteome.
SQ SEQUENCE 252 AA; 26720 MW; F1F445AB82C2DBDE CRC64;

Query Match 27.2%; Score 355; DB 16; Length 252;
Best Local Similarity 35.1%; Pred. No. 1.1e-16;
Matches 94; Conservative 40; Mismatches 100; Indels 34; Gaps 7;
QY 8 VKGIIVITGASGGLTAERLVGGASAVLLDLPN-----SGGEAQAARKLG 55
DB 3 LKDKVITITGGCGGRAMGELTLAGKARLVDINRERDEAVAACKAAGDRA---- 58
QY 56 NNVEVAPADVTSEKVDQATALALAKGFRGVAVNACAGIAVSKTYLKKGQTH- TLED 113
DB 59 -----YVCNVADEQVTHVMAQVAVSDFGAINGLVNNAGILRDGLTIKKDQSLKMSLAQ 113
QY 114 FQRIIVDLVNLGTFENIRIVAGEMQ--NEPDGQGRGVIINTASVAEFEGVQAAYASAS 171
DB 114 WQSVIVDLVNLGTFCTREVAAMKIELNE-----GAVIVISSISR-AGNMGASNSAA 165
QY 172 KGGIVGMLPIARLDAPIGIRMTAPGLFTPLTSLPEKVCNFIASQVFPSPRLGPPA 231
DB 166 KAGVADPFWAKKELARIGIRVAGVAPGFIEETEMTAGKPPALEKMTGIPPL-KRMGPV 224
QY 232 EYAHVQAIEMPFINGEYIRLDGAIIM 259
DB 225 ETASVAVIIFENDYTGRTVLELDGSLRL 252

RESULT 21
Q97DA6 PRELIMINARY; PRT; 249 AA.
AC 097DA6;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE 3-oxoacyl-acyl carrier protein reductase.
GN CAC3574.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1486;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11465286;
RA Neolling J., Breton G., Ometchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hittl J., Wolf Y.I.,
Ratusov R.L., Sabetie F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.,
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).

DR EMBL; AF007854; AAK81497.1; -
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 249 AA; 26247 MW; B13D7EDAC1A626A CRC64;

Query Match 26.3%; Score 343.5; DB 16; Length 249;
Best Local Similarity 33.2%; Pred. No. 6.3e-16;
Matches 86; Conservative 56; Mismatches 96; Indels 21; Gaps 6;
QY 8 VKGIIVITGASGGLTAERLVGGASAVLLDLPNSGGEAQA-----AKRLGNVVPAP 62
DB 5 LSGKVAIVTGAAGRGRLALALAAEGANLV-VNTRSSAEFTQKLEIEELGSAVAVK 63
QY 63 ADVTSEKVDQATALALAKGFRGVAVNACAGIAVSKTYLKKGQTHLEDFQRLVDNL 122
DB 64 ADISKYDEAEITIKKALDEYGVTDIVNNAGITKDLNLRKE-----EDFDSVINVNL 117
QY 123 MGFENIRLVAGEMGNEPDGQGRGVIINTASVAEFEGVQAAYASAKSGIVGMLPI 182
DB 118 KGFNFCKIKHTRVMLKK-----KSGKITISSVIGLIGNAQVYMAAKAGIIMTSV 171
QY 183 ARDLAPIGIRMTAPGLFTPLTSLPEKVCNFIASQVFPSPRLGPPAFAHVAITIE 242
DB 172 AKELASRGITVNVNAGIISKDMDTALTDKORESIIVAAVPL-NKVGAEADVAVNLVFLAS 230
QY 243 --NPFINGEYIRLDGAIIM 259
DB 231 DLSSYITGOVINVDGQVM 249

RESULT 22
Q42774 PRELIMINARY; PRT; 297 AA.
AC 042774;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 3-oxoacyl-[acyl-carrier-protein]-reductase.
GN OAR-1 OR B2A19.180.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariiales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Buerger F., Brors B., Welts H.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte U., Algn V., Hohnsels J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Kewes H.W., Mannhaupt G.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
CC EMBL; AF042860; AAB9799.1; -
DR EMBL; AL330092; CAB98248.1; -
DR HSSP; O70351; 1B6W.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR OXIDOREDUCTASE.
KW OXIDOREDUCTASE.
SQ SEQUENCE 297 AA; 31342 MW; 8DC08FEDF564196F CRC64;

QY	254	DGAIRM	259
Db	247	DGALRM	252
RESULT	13		
Q80F12			
ID	Q80F12	PRELIMINARY;	PRT: 257 AA.
AC	Q80F12		
DT	01-JUN-2002	(TREMBLrel, 21, Created)	
DT	01-JUN-2002	(TREMBLrel, 21, Last sequence update)	
DT	01-JUN-2002	(TREMBLrel, 21, Last annotation update)	
DE	3-hydroxacyl-CoA dehydrogenase type II.		
GN	ATU1415 OR AGR_C.2613.		
OS	Agrobacterium tumefaciens (strain C58 / ATCC 33970).		
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;		
OC	Rhizobiaceae; Rhizobium.		
OX	NCBI_TaxID=176239;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21608550; PubMed=11743193;		
RA	Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,		
RA	Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,		
RA	Chen Y., Paulsen I.T., Eilen J.A., Karp P.D., Bovee D. St.,		
RA	Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,		
RA	Kuyavayn T., Levy R., Li M.-J., McCelland E., Palmieri A.,		
RA	Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,		
RA	Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,		
RA	Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,		
RA	Chumley F., Tingey S.V., Tomb J.F., Gordon M.P., Olson M.V.,		
RA	Nester E.W.;		
RT	"The genome of the natural genetic engineer Agrobacterium tumefaciens		
RL	C58.";		
RL	Science 294:2317-2323(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21608551; PubMed=11743194;		
RA	Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,		
RA	Houmel K., Gordon J., Vaudin M., Tatchouk O., Epp A., Millin L.,		
RA	Wollam C., Allinger M., Doughy D., Scott C., Lapps C., Martelz B.,		
RA	Flanagan C., Crowell C., Gouson J., Lomo C., Sear C., Strub G.,		
RA	Cielo C., Slater S.;		
RT	"Genome sequence of the plant pathogen and biotechnology agent		
RL	Agrobacterium tumefaciens C58.";		
RL	Science 294:2323-2328(2001).		
DR	EMBL; AE009102; AAL4242.1;		
DR	EMBL; AE008067; AAK87207.1;		
KW	Complete proteome.		
SC	SEQUENCE 257 AA; 26622 MW; FF74A61FEC4B2B5C CRC64;		
Query Match	49.2%; Score 642; DB 16; Length 257;		
Best Local Similarity	51.7%; Pred No. 3.6e-36;		
Matches 134; Conservative	41; Mismatches 76; Indels 8; Gaps 3		
QY	7	SVKGLVAVITGASGLGATATRLVYOGGASAVLLDLPNSGGEAQAQKIGNNVFAPADVT	66
Db	2	NEGAGALVATGASGLGATATRLVYOGGASAVLLDLPNSGGEAQAQKIGNNVFAPADVT	59
QY	67	SEKDVOTATLAKGFEGRDVAVNAGTAVASKTYNLKKGGQHTLEDDPQVLDVNLGTF	126
Db	60	SNADQQAATKVAASAKGIRILVNCAGISTAGRI--LGEFGPOPLEDFOVIRVNLIGTF	117
QY	127	NVIRLVAGMGONEPDG---GARGVINTASVAAFEGQVQAAYASASKSGIVGNTLPT	182
Db	118	NMRLAAAHMAREDEGODSRQDNGVIYNTASVAFAFEGQICQAAYAAASKGIVSIALPA	177
QY	183	ADLAPIGIRVNTTATGPGTEPLTSLPKYCNFLASQVFPFPRIGDPREVAHVGAAITE	242
Db	178	ABELLAERIRVNTVAPGIRLPLTGLGPEVGEISLAGQIPHSRLSDPPEAFATVFFLE	237

Oy	243	NPFNGEYIRLDGAIRMOP	261
		:::	
Dd	238	NDIMAGEYIRLDGAIRMOP	256

RESULT 14			
O9DCX5	ID	PRELIMINARY:	PRT: 126 AA.
AC	O9DCX5		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Hydroxycyl-coenzyme A dehydrogenase, type II.		
GN	HSD17B10 OR HADH2.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=KIDNEY;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shitagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi S., Fukuoka S.,		
RA	Aizawa K., Izawa M., Niehi K., Kiyosawa H., Kondo S., Yamamaka I.,		
RA	Salto T., Okazaki Y., Gojibori T., Bono H., Kasakawa T., Salto R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant F.,		
RA	Fledschmann W., Gaasterland T., Gissi C., King B., Kochava H.,		
RA	Kuehl P., Lewis S., Matsumo Y., Nikiado I., Pesole G., Quackenbush J.,		
RA	Schimi L.M., Stubi F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Oikido T., Furuno M., Anco H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.T., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustincich S., Hill D., Hofman M., Hume D.A., Kamuya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,		
RA	Norione P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,		
RA	Hayashizaki Y.;		
RL	*Functional annotation of a full-length mouse cDNA collection.*;		
RL	Nature 409:685-690(2001).		
-I-	SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES		
CC	(SDR) FAMILY.		
DR	EMBL; AK002368; BAB22046.1; -		
DR	HSSP; C70351; LE6W.		
DR	MGP; MG1:133871; Hsd17b10.		
DR	InterPro: IP002198; ADH.short.		
DR	Pfam: PF00106; adh_short.1.		
DR	PRINTS; PR00080; SDRFAMILY.		
DR	PROSITE; PS00061; ADH_SHORT; 1.		
KW	Oxidoreductase.		
SQ	SEQUENCE 126 AA: 13265 MW: 78FFB6D441B9989D CRC64;		

Query Match	46.5%	Score 607;	DB 11;	Length 126;
Best Local Similarity	95.2%;	Pred No. 3,7e-34;		
Matches 120;	Conservative 2;	Mismatches 4;	Indels 0;	Gaps 0

Oy	136	MCONEPDGCGRGVINTASVAAFEGVGQAASAKSGIGVTLPDIARDLADIGIRVMT	195
Dd	1	MCONEPDGCGRGVINTASVAAFEGVGQAASAKSGIGVTLPDIARDLADIGIRVMT	60
Oy	196	IAPGLFGTLLSLPEKVCNPLASGVPPFSRAGDPAEVAHLVQALLENPLNEVRILDS	255
Dd	61	IAPGLFAITLTTPKVNPLASGVPPFSRLDPAEVAHLVOTIIENPFLNEVIRLDG	120
Oy	256	AIRMOP 261	
Dd	121	AIRMOP 126	

RESULT 15

```
QY 123 MGFENVRLVAGEMGNEPDGQGVYINTASVAFAEGVGQAAYSASKSGIVGMLPT 182
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 120 LGTFNVIRHGVALLMGEHEKMDANGRGVYINTASVAFAEDGQGSAYSASKGVYGMPL 179
QY 183 ARDIAPGIRVMTIAPGLFGTPLLTSPEKYCNFLASQVPPPSRLGDPAEYAHVQAIIIE 242
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 180 ARDEAGGIRVMTIAPGLMDTPLLSTPEKYSFIAQLIPNPSRLGHPHEYGALVQHIIIE 239
QY 243 NPFNGEYIRLDGAIRM 259
    |  ||||  |||  |||  |||
DB 240 NGYNGEYIRFDGALRM 256
```

RESULT 6

```
Q910T0 PRELIMINARY; PRT; 255 AA.
ID 0910T0
AC 0910T0:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Probable short-chain dehydrogenase.
GN PA2554.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
NCBI_TaxID=287;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wedman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lathin K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reiter J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.,
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
    (SDR) FAMILY.
DR EMBL: AE004683; AAC05942.1; -
DR HSPF: 070351; IE83.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KM Oxidoreductase; Complete proteome.
SEQUENCE 255 AA; 26426 MW; EB8FF28712D2936D CRC64;
```

```
Query Match 55.2%; Score 720; DB 16; Length 255;
Best Local Similarity 57.5%; Pred. No. 1.8e-41;
Matches 145; Conservative 39; Mismatches 66; Indels 2; Gaps 1;
QY 8 VKGLAVITGASGLGATAERLVGGASAVLLDLPNSGGEAOKKLGNNVFPADYVS 67
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 3 IENRFVLTGSSGSGATKAVLQSGKVTADINAEAGAKAEELGAKRFRAIDIAS 62
QY 68 EKDVOITALAKKGFGRVDVAVNCAGIAVASKTYNLKKQTHLTEDFORVLDVNLMTFN 127
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 63 EADGQAAVAALAEAFGGHGLANCAGVAPAEKV--LGRNGIHAILESFRRVIDINLVGSFN 120
QY 128 VIRLVAGEMGNEPDGQGVYINTASVAFAEGVGQAAYSASKSGIVGMLPTIARDLA 187
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 MRLAAEAMAKNPPGGGEGVYINTASVAFAEDGIGQAAYSASKSGVAGMLTPARELA 180
QY 188 PIGIRVMTIAPGLFGTPLLTSPEKYCNFLASQVPPPSRLGDPAEYAHVQAIIENPFLN 247
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 181 REGIRVMTIAPGLFGTPLLTSPEKYCNFLASQVPPPSRLGDPAEYAHVQAIIENPFLN 240
QY 248 GEVIRLDGAIRM 259
    |||||:|||||
DB 241 GEVIRLDGAIRM 252
```

RESULT 7

```
Q8YBS0 PRELIMINARY; PRT; 255 AA.
ID 08YBS0
AC 08YBS0:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 3-oxoacyl-(acyl-carrier protein) reductase (EC 1.1.1.100).
GN BME10816.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
NCBI_TaxID=29459;
RX MEDLINE=20020109; PubMed=11756688;
RA Delvecchio V.G., Kapural V., Redkar R.J., Patra G., Muter C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykakis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL: AE009715; AAL54058.1; -
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KM Oxidoreductase; Complete proteome.
SEQUENCE 255 AA; 26263 MW; 5CF61DAB37F6B730 CRC64;
```

```
Query Match 54.5%; Score 711; DB 16; Length 255;
Best Local Similarity 57.1%; Pred. No. 7.4e-41;
Matches 144; Conservative 37; Mismatches 69; Indels 2; Gaps 1;
```

```
QY 8 VKGLAVITGASGLGATAERLVGGASAVLLDLPNSGGEAOKKLGNNVFPADYVS 67
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 3 IENRFVLTGSSGSGGLAANVSKAVEAGKAVLLDVAAEGEAGKALGSAFQRIDVAS 62
QY 68 EKDVOITALAKKGFGRVDVAVNCAGIAVASKTYNLKKQTHLTEDFORVLDVNLMTFN 127
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 63 DTGKAAIAAIAEAFSRIDVLVNCAGVAPAEKV--LGRGAHKLTFRTTISINLIGFN 120
QY 128 VIRLVAGEMGNEPDGQGVYINTASVAFAEGVGQAAYSASKSGIVGMLPTIARDLA 187
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 MRLAAEAMAKNPPGGGEGVYINTASVAFAEDGIGQAAYSASKSGVAGMLTPARELA 180
QY 188 PIGIRVMTIAPGLFGTPLLTSPEKYCNFLASQVPPPSRLGDPAEYAHVQAIIENPFLN 247
    |||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 181 RHGIRVMTIAPGLFGTPLLTSPEKYCNFLASQVPPPSRLGDPAEYAHVQAIIENPFLN 240
QY 248 GEVIRLDGAIRM 259
    |||||:|||||
DB 241 GEVIRLDGAIRM 252
```

```
RESULT 8
Q8XWEO PRELIMINARY; PRT; 252 AA.
ID 08XWEO
AC 08XWEO:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Probable 3-hydroxyacyl-CoA dehydrogenase type II oxidoreductase
    protein (EC 1.1.1.35).
GN RSC2534 OR RS05766.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
Ralstonia.
```

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Bocfeld D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guttingich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shiba Y., Storch K.-F.,
 RA Suzuki H., Teyo-Oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseuk S.,
 RA Hayashizaki Y.,
 RA "Functional annotation of a full-length mouse cDNA collection";
 RT Nature 409:685-690(2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 RL
 CC (SBR) FAMILY
 DR EMBL: AK013340; BAB28800.1; -
 DR HSSP: O70351; IEGW.
 DR MGD: MGI:1333671; Hsd17b10.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KM Oxidoreductase.
 SQ SEQUENCE 261 AA; 27273 MW; F36CD19C7FCEFAF CRC64;

Query Match 87.7%; Score 1143; DB 11; Length 261;
 Best Local Similarity 87.0%; Pred. No. 3.6e-70;
 Matches 227; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLGATATRLVGGASAVLDLPNSGGGAOKKGNVVF 60
 DB 1 MAARVSYKGLVAVITGASGLGATATRLVGGASAVLDLPNSGGGAOKKGNVVF 60
 QY 61 APADVTSEKDVOTATLALAKGKFGKRVDAVNCAGIAVASKTYNLKGGHTLEDFORVLDV 120
 DB 61 APANTSEKELQALTLAKKEFGKRDVAVNCAGIAVAKTYHOKKNTHTLEDFORVINV 120
 QY 121 NLMGTFTNIRLVAGMGONPEPDGQGRVITNTASVAEFESQVQAAVSASKSGIVGKTL 180
 DB 121 NLTGTFNIRLVAGMGONPEPDGQGRVITNTASVAEFESQVQAAVSASKSGIVGKTL 180
 QY 181 PIARDLAFIGIRVMTIAPGLFGTPLTSLPEKVCNFTLASGVFPFSRLDPEVAHLVOAI 240
 DB 181 PIARDLAFIGIRVMTIAPGLFGTPLTSLPEKVCNFTLASGVFPFSRLDPEVAHLVOAI 240
 QY 241 IENPFLNGEVIIRLDGAIIRMP 261
 DB 241 IENPFLNGEVIIRLDGAIIRMP 261
 RESULT 4
 QY 08TCV9 PRELIMINARY; PRT; 196 AA.
 AC 08TCV9;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Endoplasmic reticulum-associated amyloid beta peptide-binding protein (Fragment).
 GN ERAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Delinger M.H., Weyermann R., Schluesener H.J.:
 RT "Expression, release and induction of endoplasmic reticulum-associated amyloid beta-binding protein in brain disease";
 RT Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases

DR EMBL: AY092415; AAM18189.1; -
 FT NONTER 196 1
 SQ SEQUENCE 196 AA; 20581 MW; 2400DE14966BA6A CRC64;
 Query Match 75.4%; Score 983; DB 4; Length 196;
 Best Local Similarity 99.5%; Pred. No. 1.8e-59;
 Matches 195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 51 AKRLGNVYFAPADVTSEKDVOTATLALAKGKFGKRVDAVNCAGIAVASKTYNLKGGHT 110
 DB 1 AKRLGNVYFAPADVTSEKDVOTATLALAKGKFGKRVDAVNCAGIAVASKTYNLKGGHT 60
 QY 111 LEDFORVLDVNLMTFTNIRLVAGMGONPEPDGQGRVITNTASVAEFESQVQAAVSA 170
 DB 61 LEDFORVLDVNLMTFTNIRLVAGMGONPEPDGQGRVITNTASVAEFESQVQAAVSA 120
 QY 171 SKGGIVGKTLPIARDLAFIGIRVMTIAPGLFGTPLTSLPEKVCNFTLASGVFPFSRLD 230
 DB 121 SKGGIVGKTLPIARDLAFIGIRVMTIAPGLFGTPLTSLPEKVCNFTLASGVFPFSRLD 180
 QY 231 AEYAHVQAIIENPFL 246
 DB 181 AEYAHVQAIIENPFL 196

RESULT 5
 ID 019102 PRELIMINARY; PRT; 258 AA.
 AC 019102;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Probable 3-hydroxyacyl-CoA dehydrogenase F01G4.2 type II (EC 1.1.1.35)
 DE (Type II HADH).
 GN F01G4.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 CC Rhabditidae; Peloiderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Harris B.;
 RT Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA + NADH.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 RL
 CC (SBR) FAMILY
 DR EMBL: Z68341; CA92764.1; -
 DR HSSP: O70351; IEGW.
 DR WormPep: F01G4.2; CE03127.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KM Hypothetical protein; Oxidoreductase; NAD; Mitochondrion.
 FT NP_BIND 11 36
 FT ACT_SITE 165 165
 SQ SEQUENCE 258 AA; 27143 MW; 86BF2568EE5902B3 CRC64;

Query Match 57.4%; Score 748; DB 5; Length 258;
 Best Local Similarity 59.9%; Pred. No. 2.3e-43;
 Matches 154; Conservative 34; Mismatches 67; Indels 2; Gaps 1;

QY 3 AACRSYKGLVAVITGASGLGATATRLVGGASAVLDLPNSGGGAOKKGNVVFAP 62
 DB 2 SALRSTGGLVAVITGASGLGATATRLVGGASAVLDLPNSGGGAOKKGNVVFAP 59
 QY 63 ADVTSEKDVOTATLALAKGKFGKRVDAVNCAGIAVASKTYNLKGGHTLEDFORVLDV 122
 DB 60 ASVTSEKDVOTATLALAKGKFGKRVDAVNCAGIAVASKTYNLKGGHTLEDFORVLDV 119

90 286.5 22.0 254 16 Q92PP8 rhizobium m
91 286 21.9 275 16 Q9K4H0 09k4h0 streptomyc
92 285.5 21.9 254 16 Q9R4H0 09r4h0 streptomyc
93 285 21.9 255 16 Q9PCO2 09pc02 xyella fas
94 284.5 21.8 257 16 Q9WYD3 09wyd3 thermotoga
95 284 21.8 240 16 Q9AAT3 09aat3 caulobacter
96 283.5 21.7 256 17 Q8TTL5 08ttl5 methanosarc
97 283 21.7 252 16 Q92PP0 092pp0 rhizobium m
98 282.5 21.7 253 16 Q9CH41 09ch41 lactococcus
99 282.5 21.7 272 16 Q9RGI1 09rgi1 staphylococ
100 282.5 21.7 521 16 Q9AT99 09at99 caulobacter

ALIGNMENTS

RESULT 1

ID Q96HDS PRELIMINARY; PRT; 252 AA.
AC Q96HDS;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DR 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Similar to hydroxacyl-coenzyme A dehydrogenase, type II.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strusberg R.;
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL: BC008708; AA008708.1; -;
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 252 AA; 25984 MW; F36B71070CE872D CRC64;

Query Match 95.1%; Score 1240.5; DB 4; Length 252;

Best Local Similarity 96.2%; Pred. No. 8.3e-77;

Matches 251; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

QY 1 MAAACRSYKGLVAVITGGASGLGATAEFLVGGASAVLLDLPNSGGEAQAQKLGNNVF 60
DB 1 MAAACRSYKGLVAVITGGASGLGATAEFLVGGASAVLLDLPNSGGEAQAQKLGNNVF 60
QY 61 APADVTSEKVOYOTALAKKGFGRVDVAVNCAGIYVASKTYNKKGCTHTLEDFORVLDV 120
DB 61 APADVTSEKVOYOTALAKKGFGRVDVAVNCAGIYVASKTYNKKGCTHTLEDFORVLDV 120
QY 121 NMGTFENVIRLVAGEMQNEPDGQGVIIINTASVAAFEFGVGAASASKGIYGMTL 180
DB 121 NMGTFENVIRLVAGEMQNEPDGQGVIIINTASVAAFEFGVGAASASKGIYGMTL 180
QY 121 NMGTFENVIRLVAGEMQNEPDGQGVIIINTASVAAFEFGVGAASASKGIYGMTL 180
DB 121 NMGTFENVIRLVAGEMQNEPDGQGVIIINTASVAAFEFGVGAASASKGIYGMTL 180
QY 181 PIARDLAPGIRVMTIAPGLFTPLTSLPEKVCNFLASQVPPSRLGPAEYAHLVQAI 240
DB 181 PIARDLAPGIRVMTIAPGLFTPLTSLPEKVCNFLASQVPPSRLGPAEYAHLVQAI 240
QY 181 PIARDLAPGIRVMTIAPGLFTPLTSLPEKVCNFLASQVPPSRLGPAEYAHLVQAI 240
DB 181 PIARDLAPGIRVMTIAPGLFTPLTSLPEKVCNFLASQVPPSRLGPAEYAHLVQAI 240
QY 241 IENPFLNGEYIRLDGAIKMP 261
DB 241 IENPFLNGEYIRLDGAIKMP 261
QY 232 IENPFLNGEYIRLDGAIKMP 252
DB 232 IENPFLNGEYIRLDGAIKMP 252

RESULT 2
Q99N15 PRELIMINARY; PRT; 261 AA.
ID Q99N15;
AC Q99N15;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Short chain L-3-hydroxyacyl-CoA dehydrogenase.
GN HSD17B10 OR SCHAD.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21098701; Pubmed=11165016;
RA He X.Y., Metz G., Chu C.H., Lin D., Yang Y.Z., Mehra P., Schulz H.,
RA Yang S.Y.,
RT Molecular cloning, modeling, and localization of rat type 10 17beta-
RT hydroxysteroid dehydrogenase.";
RL Mol. Cell. Endocrinol. 171:89-98(2001).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL: AF233685; AAK15008.1; -;
DR HSSP: C70351; 1E6W.
DR MGD; MG1:133871; Hsd17b10.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 261 AA; 27273 MW; F371ED8A15FCFAF CRC64;

Query Match 88.0%; Score 1147; DB 11; Length 261;

Best Local Similarity 87.4%; Pred. No. 1.9e-70;

Matches 228; Conservative 18; Mismatches 15; Indels 0; Gaps 0;

QY 1 MAAACRSYKGLVAVITGGASGLGATAEFLVGGASAVLLDLPNSGGEAQAQKLGNNVF 60
DB 1 MAAACRSYKGLVAVITGGASGLGATAEFLVGGASAVLLDLPNSGGEAQAQKLGNNVF 60
QY 61 APADVTSEKVOYOTALAKKGFGRVDVAVNCAGIYVASKTYNKKGCTHTLEDFORVLDV 120
DB 61 APADVTSEKVOYOTALAKKGFGRVDVAVNCAGIYVASKTYNKKGCTHTLEDFORVLDV 120
QY 121 NMGTFENVIRLVAGEMQNEPDGQGVIIINTASVAAFEFGVGAASASKGIYGMTL 180
DB 121 NMGTFENVIRLVAGEMQNEPDGQGVIIINTASVAAFEFGVGAASASKGIYGMTL 180
QY 121 NMGTFENVIRLVAGEMQNEPDGQGVIIINTASVAAFEFGVGAASASKGIYGMTL 180
DB 121 NMGTFENVIRLVAGEMQNEPDGQGVIIINTASVAAFEFGVGAASASKGIYGMTL 180
QY 181 PIARDLAPGIRVMTIAPGLFTPLTSLPEKVCNFLASQVPPSRLGPAEYAHLVQAI 240
DB 181 PIARDLAPGIRVMTIAPGLFTPLTSLPEKVCNFLASQVPPSRLGPAEYAHLVQAI 240
QY 241 IENPFLNGEYIRLDGAIKMP 261
DB 241 IENPFLNGEYIRLDGAIKMP 261

RESULT 3

Q9CYT3 PRELIMINARY; PRT; 261 AA.

ID Q9CYT3;
AC Q9CYT3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hydroxyacyl-coenzyme A dehydrogenase, type II.
GN HSD17B10 OR HADH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,


```
XX 17-JUL-1995; 95WC-GB01678.
PF
XX 20-JUL-1994; 94GB-0014622.
PR
XX ( ZENE ) ZENECA LTD.
PA
XX Chase D, Elborough K, Fentem PA, Siabas AR, White A;
XX WPI: 1996-105914/11.
DR N-PSDB; AAG99304.
XX
XX New isolated rape beta-ketoreductase DNA - used to develop plants
XX with lower or higher oil contents or with altered oil compsn.
XX
XX Claim 1; Page 15; 29pp; English.
XX
CC The sequence corresponds to a rape seed beta-ketoreductase encoded
CC by a cDNA insert in plasmid pRS10.1 in Escherichia coli X11-Blue.
CC A plastid stroma targeting transit peptide is present. DNA
CC encoding the protein may be inserted in a vector or expression
CC cassette in sense or antisense orientation for expression in an
CC oilseed plant, e.g. for production of transgenic rape plants with
CC low or modified oil content, diversion of metabolism to alternative
CC storage compounds, e.g. starch, protein or engineered polymers, or
CC production of plants with enhanced oil content. The DNA may also
CC be used as a probe to obtain similar genes from other plants. The
CC transit peptide may be used to direct other proteins to seed
CC plastids.
XX
SQ Sequence 315 AA:
Query Match 22.7%; Score 296; DB 17; Length 315;
Best Local Similarity 30.9%; Pred. No. 5,8e-20;
Matches 81; Conservative 44; Mismatches 115; Indels 22; Gaps 6;
QY 4 AVRSYKGLVAVITGASGLGATATRLVGOGASAVLLDLPNSGGEA-----QAKRLGNMC 58
Db 66 AVKVESPPVYVVGASGSGIKATLSTL-GKAGCKVLVNTARSAAKEAEVSKQIEAYGGQA 124
QY 59 VEPADVTSKEDYQTLALAKGKFGRYDAVNCAGTAVASKTYNLKKGQTHLEDFQRYL 118
Db 125 IIFGGDVSKEDAEAMKTAIDAMGTIDVYVNNAGITRDLLIRMKRSQ-----WDEVY 178
QY 119 DVNLMGTFNVIRLVAGEMGQNEPDGQGVIIINTASVAFAEGOVGOAAVSASGSGIVGM 178
Db 179 DLNLITGVFLCTQAATKIMMK-----RKRIITINIASVGLIGNIGQANTAAAKAGVIGF 232
QY 179 TLPIARDLAPIGIRVMTIAPGLFTPLLSLPKVCNCFLASQVPPSPRLGDPAEYAHVQ 238
Db 233 SKTAARAGSARNTINNVNVCPCGFITASDMTAKIGDMKKIILGIPL-GRYGQPEDVAGLVE 291
QY 239 AIIENP---FLNGEVIRLDGAI 257
Db 292 FLALSPAASTIITGCAFTIDGCI 313
```

Search completed: June 23, 2003, 14:28:28
Job time : 41.6667 secs

XX 18-DEC-2001 (first entry)
 DT Novel human secretory protein, Seq ID No 653.
 DE
 XX Human: secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200166689-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001, 2001MO-US04942.
 XX
 PD 07-MAR-2000, 2000US-0519705.
 PR 19-MAR-2000, 2000US-0574454.
 PR 17-JUN-2000, 2000US-0596193.
 PR 14-JUL-2000, 2000US-0616847.
 PR 19-SEP-2000, 2000US-0655363.
 PR 20-OCT-2000, 2000US-0693267.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P,
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 XX
 DR N-PSDB; AAS45196.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 XX
 PS Example 2; SEQ ID No 653; 107pp; English.
 XX
 CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catalolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides

CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention.
 XX
 SQ Sequence 288 AA;
 Query Match 23.1%; Score 301.5; DB 22; Length 288;
 Best Local Similarity 29.9%; Pred. NO. 1.5e-20;
 Matches 84; Conservative 44; Mismatches 110; Indels 43; Gaps 6;
 QY 1 MAAAVRSYKGLVAVITGASGLGATATRLVGGASAVLIDLPSNGEPAQRKLGNNCVF 60
 DB 10 MATGTR-YAGKVAAYVTGGGRCIGAGIVAFVNSGARVYCDKDESGRALQELPGCLL 68
 QY 61 APADYTSKDYQVATLALKGKRGYDVAVNCAGIAVASKITNLRKGGHTLEDFORYLDV 120
 DB 69 SCDVYQEDDVKKTIVSETIRRRGRUDCVNNAHHPPP-----QRPETSAHGRQLEL 123
 QY 121 NLMGTENVIRLVAGMGQNEPDGQRCVVIINTASVAAFEGOVQAAVSASKGIVGNTL 180
 DB 124 NLGTYTLTKLALPYLRKSQ-----GNVINISLVGATGQAQAVPVATKGAVTAMTK 176
 QY 181 PIARDLPIGIRVMTIARGLFTPLTSLPEKVCNPLASQVFPF----- 224
 DB 177 ALALDESPGVKAVNCISGNTWTPLEW-----LALMPDPATIREGMLAQRSGV 228
 QY 225 -----SRUGDPAEY-AHLVQALTEENPFLNGEYIRLDGAIM 259
 DB 229 QIQPLGRMGQPAEYGAAGVFLASEANFCTGIXLTLVTGAEL 269
 RESULT 23
 ID AAY95746 standard; Protein; 247 AA.
 XX
 AC AAY95746;
 XX
 DT 25-OCT-2000 (first entry)
 XX
 DE Bacillus megaterium 3-keto-acyl-CoA reductase Phab.
 XX
 KW Polyhydroxyalkanoate; polyhydroxybutyrate; transgenic plant; Phab;
 KW 3-keto-acyl-CoA reductase.
 XX
 OS Bacillus megaterium.
 XX
 PN WO200040730-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 07-JAN-2000, 2000MO-US00364.
 XX
 PR 07-JAN-1999, 99US-0115592.
 XX
 PA (UYMA-) UNTV MASSACHUSETTS.
 XX
 PI Cannon MC, Cannon FC, Mccool GJ, Valentin HE, Gruys KJ;
 XX
 DR WPI: 2000-532624/48.
 DR N-PSDB; AAS50142.
 XX
 PT New nucleic acid fragment encoding proteins involved in
 PT polyhydroxyalkanoate (PHA) biosynthesis, useful in the production of
 PT transgenic plants or recombinant plant cells which can express PHAs
 PT such as polyhydroxybutyrate -
 XX
 PS Claim 85; Page 137-138; 153pp; English.
 XX
 CC The present sequence is that of Phab, a 3-keto-acyl-CoA-reductase
 CC protein of Bacillus megaterium. The sequence was deduced from an
 CC open reading frame identified in an isolated 7,916 bp fragment of
 CC B. megaterium strain 11561 genomic DNA (see AAS50142). The 7,916 bp

PR 05-APR-1999; 990P-0098205.
XX
PA (DAIL) DAICEL CHEM IND LTD.
XX
PI Yamamoto H;
XX
DR WPI: 2000-118183/11.
XX N-PSDB; AA245749.
XX
PT Producing optically pure (S)-4-halo-3-hydroxybutyric acid ester -
XX
PS Claim 6; Page 19-20; 34pp; English.
XX
CC The present sequence represents a beta-ketoacyl-ACP reductase protein
CC of bacillus subtilis. The beta-ketoacyl-ACP reductase enzyme constitutes
CC a Type II fatty acid synthetase. The enzyme has an extremely high
CC reducing activity and stereoselectivity towards 4-chloroacetoacetic
CC acid ester. The specification describes a method for producing a
CC (S)-4-halo-3-hydroxybutyric acid ester. The method comprises
CC asymmetrically reducing 4-halo-acetoacetic acid ester or its
CC derivative with beta-ketoacyl-acyl carrier protein reductase
CC constituting Type II fatty acid synthase, or acetoacetyl-CoA
CC reductase constituting the polybeta-hydroxy fatty acid biosynthesis
CC system. The novel method is used to produce optically active
CC 4-halo-3-hydroxybutyric acid ester, with a high purity.
XX
SQ Sequence 248 AA;

Query Match 23.8%; Score 310.5; DB 21; Length 248;
Best Local Similarity 29.7%; Pred. No. 1.7e-21;
Matches 76; Conservative 55; Mismatches 100; Indels 25; Gaps 6;

QY 13 AVITGGASGLGATLAEERLVGQASAVLLDLPNSGGEAQA-----KRLGNNCVAPADY 65
DB 9 AATGASRSGISIALALAKSGANV---VNSGNEAKNEVDEIKSGRAIAVKADY 65
QY 66 TSEKDVQTLALAKGFRGVADVAVNCAGIAVASKTYNLKKGOTHLLEPDRPLDNLNGI 125
DB 66 SNEDEVQNNIKETLSFTSTIDILVNNAGITRDLNLRKKE-----DEMDDVYINLNGV 119
QY 126 FNVIRLVAGEGQNEPDGQGRGVIIINTASVAFAEGVQQAASASKGIVGMLPIARD 185
DB 120 FNCTKAVTRQMKQ-----RSGRIINSSIVGSGNPGQANYVAAKAGVIGLTRKSAKE 173
QY 186 LAPIGRVMTIAPGLGFTPLSLPEKVCNFIASQVPPSRIGDPAEVAHIVQALIEEN-- 243
DB 174 LMSRNTVVAIAAPGISTDMTDLKADVDENMLKQIPL-ARGGEPSDVSSVYTFLASGA 232

QY 244 PFLNGEVIRLDGAIRM 259
DB 233 RYMTGOTLHDGGMV 248

RESULT 21
ABBA8892
ID ABBA8892 standard; Protein; 247 AA.
AC ABBA8892;
XX
XX 05-FEB-2002 (first entry)
XX
XX Listeria monocytogenes protein #1596.
XX
XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
XX vitamin B12; bacterial infection; disease.
XX
XX Listeria monocytogenes.
XX
XX WO200177335-A2.
XX
XX 18-OCT-2001.
XX
XX 11-APR-2001; 2001WO-FR01118

XX
PR 11-APR-2000; 2000FR-0004629.
XX
PA (INSP) INST PASTEUR.
XX
PI Buchrieser C, Frangoul L, Couve E, Rusniok C, Faht H, Dehoux P;
PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kieft J, Kunh M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tleier-Hartinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Chardit A, Durant L;
PI Perez-Diaz J, Baguero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueno E, De Padlos B, Wehland J, Kaerst U, Ertlan K, Hauf J;
PI Rose M, Voss H;
XX
DR WPI: 2002-010914/01.
XX
XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
XX and prevention of Listeria and related bacterial infections, and
XX related polypeptides -
XX
PS Claim 6; SEQ ID No 1597; 192pp; French.
XX
CC The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see AB03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 247 AA;

Query Match 23.3%; Score 303.5; DB 23; Length 247;
Best Local Similarity 32.0%; Pred. No. 8.1e-21;
Matches 85; Conservative 45; Mismatches 103; Indels 33; Gaps 7;

QY 7 SVKGLAVITGGASGLGATLAEERLVGQASAVLLDLPNSGGEAQA-----KKL-----GNMC 58
DB 2 TLQGVAVVITGGSGRIGDIAINLAKGANIFF---NYGSPPAEETAKTALVAHEGVEV 57
QY 59 VFAPADYSEKDVQTLALAKGFRGVADVAVNCAGIAVASKTYNLKKGOTHLLEPDRPL 118
DB 58 EAKRANVAIAEDVAFKQALIERGVDILVNNAGITRDLNLRKKE-----DEMDDVI 111
QY 119 DVNLGFTFNIRLVAGEGQNEPDGQGRGVIIINTASVAFAEGVQQAASASKGIVGML 178
DB 112 NINLKGFTLCRAVSRFMKQ-----RAGKIINMASVGLIGNAGQANYVASRAGVIGL 165
QY 179 TLPIARDLAPIGIVMTIAPGLGFTPLSLPEKVCNFIASQVPPSRIGDPAEVAHIVQ 238
DB 166 TKTTARELAPRGIVNNAVAPGFTTDMTDLKADKTEKRAMAQIP-----LGAYGTEDIAN 221
QY 239 AII-----ENPFLNGEVIRLDGAIRM 259
DB 222 AVLFLASDASKYITGOTLSVDGGMV 247

RESULT 22
AAU28296
ID AAU28296 standard; Protein; 288 AA.
AC AAU28296;
XX

Best Local Similarity 32.0%; Pred. No. 7,6e-22;
Matches 81; Conservative 41; Mismatches 105; Indels 26; Gaps 5;

```
QY 12 VAVITGGASGLTAERLVGOGASAVLLDLPNSGGEAOAKLGNVCYFADPTSEKDV 71
D 4 VCAITGGSGRIGRAVAQIMARKGRALIAIRNLSEAKAAGDLGSDHLAFSCDVAKEDV 63
QY 72 QATALAKGKFGFVDVAVNCAGI-----AVASKTYNLKKGCTHTLEDFORVLVDLMTGF 126
D 64 QNTPEMEKHGRVNFVNAAGINDSLVTRKT-----EDWVSQLHTNLLGSM 112
QY 127 NVIRLVAGMGONEPDQGGQGVITNTASVAAFESQVQAAYASAKSGIVGNTLPIARDL 186
D 113 LTKKAMRAMIQ-----QGGSIVNVGSIYGLKNGNSQSVYASAKSGLVGFSRALAKEV 166
QY 187 ADIGIRVMTIAPGLFPTLSTLPEKVCNFIASQVPPSRGLDPAFVAHLVQATIENTPFL 246
D 167 AKKIRVNVVAPGPFVHTDKLKEE--HKKNIPL-GRGGETLEVAAVFLLESPTI 222
QY 247 NGEVIRLDGAIRM 259
D 223 TGHVLVVDGGLQ 235
```

RESULT 16
AAB96397
ID AAB96397 standard; Protein; 241 AA.

XX AAB96397;
XX
XX 29-OCT-2001 (first entry)

DE Putative P. abyssi dehydrogenase #8.
XX
XX Hyperthermophilic archaeon; hyperthermophilic protein.
XX
XX Pyrococcus abyssi.

XX FR2792651-A1.

XX 27-OCT-2000.

XX 21-APR-1999; 99FR-0005034.

XX 21-APR-1999; 99FR-0005034.

XX (CNRS) CNRS CENT NAT RECH SCI.
XX (IFRE-) IFREMER INST FR RECH EXPL MER.

XX Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;
XX Querellou J, Weissenbach J, Saurin W, Hellig R;

XX WPI; 2001-126236/14.

XX New nucleotide sequences isolated from Pyrococcus abyssi encode
XX proteins useful in industry -

XX Claim 7; Pages 1087-1088; 1657pp; French.

XX The present invention relates to the genomic sequence of Pyrococcus
XX abyssi (see AAB96397 and AAB4123-7) and P. abyssi proteins. P. abyssi is
XX a hyperthermophilic archaeon, which is isolated from deep-sea
XX hydrothermal vents. The present sequence is one such P. abyssi protein.
XX The proteins of the present invention have various potential industrial
XX uses, since the proteins are stable at very high temperatures, some up to
XX 110 degrees centigrade.

XX Note: This patent is in the same patent family as WO2000055062, which
XX contains additional sequences as shown in AAB99132-AAB99143,
XX AAB95903-AAB95920 and AAB66436.

XX Sequence 241 AA;

XX Query Match 24.0%; Score 313.5; DB 22; Length 241;

Best Local Similarity 35.3%; Pred. No. 8,7e-22;
Matches 91; Conservative 44; Mismatches 88; Indels 35; Gaps 8;

```
QY 8 VKGLVAVITGGASGLTAEERLVGOGASAVLLDLPNSGGEAOAKLGNVC-----VF 60
D 4 LKGVAVITGGASGRIGRAIAIEELAKRGVNVVNRN---EEBAKTEELCRQYGVETLL 60
QY 61 APADVTEKDVQATLAKGKFGFVDVAVNCAGIATYNNLKKGCTHTLEDFORVLVD 120
D 61 VKADVNSREYREKRVKVIDKFRHIDLLINNAGI--LGKI---KDLPLVDDEMDRIVSY 115
QY 121 NMGCTFNVIRLVAGMGONEPDQGGQGVITNTASVAAFESQVQAAYASAKSGIVGNTL 180
D 116 NLKGAFTVQGEVLRYM-----KKGKIVNIASIKGKGQGVGPFYASAKSGLLALTF 166
QY 181 PIARDLPIGIRVMTIAPGLFPTLSTLPEKVCNFIASQVPPSRGLD---PAFVAHLV 237
D 167 NLAHRLAP-NLVNAVAPGPDVITDMLSEKMKELIKL-----SLTGDIAPKSEVAHAV 218
QY 238 QATIENTPFLNGEVIRLDG 255
D 219 IFLLENDHITGEVITDVG 236
```

RESULT 17
AAU28156
ID AAU28156 standard; Protein; 237 AA.

XX AAU28156;
XX
XX 18-DEC-2001 (first entry)

DE Novel human secretory protein, Seq ID No 325.

XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
XX ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
XX transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
XX amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
XX ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
XX gut protection; lung; liver fibrosis; immune deficiency; infection;
XX severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
XX multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
XX fertility; analgesic; pain; antigen.

XX Homo sapiens.

XX WO200166689-A2.

XX 13-SEP-2001.

XX 05-MAR-2001; 2001WO-US04942.

XX 07-MAR-2000; 2000US-0519705.

XX 19-MAY-2000; 2000US-0574454.

XX 17-JUN-2000; 2000US-0596193.

XX 14-JUL-2000; 2000US-0616847.

XX 19-SEP-2000; 2000US-0665363.

XX 20-OCT-2000; 2000US-0693267.

XX (HUSE-) HUSEQ INC.

XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
XX Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;

XX WPI; 2001-589934/66.
XX N-PSDB; AAS45056.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries
XX prepared from various human tissues, for diagnosis and treatment of
XX cancer, neurological, inflammatory, and autoimmune disorders -

XX Example 4; SEQ ID No 325; 107pp; English.

DB 66 ADARKMIDQAIKELGSDVLYNNAGI--TODTILMKY----TEADFEKVLKVNLTGAFNM 119
 QY 129 IRLVAGEMGNEDPOGGRGVITITASYAAFEQGVQAAVSASGSGIVGTLPIARDLAP 168
 DB 120 TQSVL-----KPMKAKREGAIIKMSVYGLMGNIQANVAAASAGLIGFTKSVAREVAS 173
 QY 189 IGRVMTIAPGLFGTPLTSLPERKCNFLASQVFPSPRLGDPAEVAHLVQAIITENPRLNG 248
 DB 174 RNRVNVITAPGMIESDPTAILSDKIKETLAQIPM-KEFGQAEQVADLTFTVLAGODYLTG 232
 QY 249 EVIRLDGAIRM 259
 DB 233 QVIAIDGGLSM 243
 RESULT 11
 AAU37988 standard; Protein; 243 AA.
 ID AAU37988
 AC AAU37988;
 DT 14-FEB-2002 (first entry)
 XX Streptococcus pneumoniae cellular proliferation protein #417.
 DE Streptococcus pneumoniae cellular proliferation protein;
 XX Antisense; prokaryotic cellular proliferation protein;
 KM antibiotic; antibacterial; drug design.
 XX Streptococcus pneumoniae.
 OS
 XX WO200170955-A2.
 PN 27-SEP-2001.
 PD 21-MAR-2001; 2001WO-US09180.
 PF 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207272P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GT;
 PI Yamamoto RT, Xu HH;
 XX
 DR N-PSDB; AA555847.
 DR
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 XX Example 3; Seq ID No 13581; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 243 AA:
 QY Query Match 25.0%; Score 326.5; DB 22; Length 243;
 Best Local Similarity 35.1%; Pred. No. 5e-23;
 Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
 DB 15 ITGSGAGLIGATPATERLVGGAGASAVLIDLPNSGGE-----AQAKKLGNNCFAPADATSE 68
 DB 10 ITGSSRGIGLAIKHKFAQAGANIVL-----NSRGATSEELLAEFSNNGIKVPIISGDVSDIF 65
 QY 69 KDVTALALAKGKFGRYDAVNCAGIYASKTYNKKGGTHTLEDFOFVLDVNLKGTENV 128
 DB 66 ADARKMIDQAIKELGSDVLYNNAGI--TODTILMKY----TEADFEKVLKVNLTGAFNM 119
 QY 129 IRLVAGEMGNEDPOGGRGVITITASYAAFEQGVQAAVSASGSGIVGTLPIARDLAP 188
 DB 120 TQSVL-----KPMKAKREGAIIKMSVYGLMGNIQANVAAASAGLIGFTKSVAREVAS 173
 QY 189 IGRVMTIAPGLFGTPLTSLPERKCNFLASQVFPSPRLGDPAEVAHLVQAIITENPRLNG 248
 DB 174 RNRVNVITAPGMIESDPTAILSDKIKETLAQIPM-KEFGQAEQVADLTFTVLAGODYLTG 232
 QY 249 EVIRLDGAIRM 259
 DB 233 QVIAIDGGLSM 243
 RESULT 12
 AAU01032 standard; Protein; 243 AA.
 ID AAU01032
 AC AAU01032;
 DT 02-OCT-2001 (first entry)
 XX CFE 35 protein sequence.
 DE
 XX Antibacterial; vaccine; gene therapy; bacterial cell wall viability;
 KM CFE; CEG; Conserved Essential Gene; bacterial infection;
 KW antisense therapy; antibiotic resistance.
 XX Streptococcus pneumoniae.
 OS
 XX WO200149721-A2.
 PN 12-JUL-2001.
 PD 29-DEC-2000; 2000WO-US35604.
 PF 30-DEC-1999; 99US-0174089.
 PR
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX Dougherty TJ, Pucci MJ, Dougherty BA, Davison DB, Brucoleri RE;
 PI Thanassi JA;
 XX
 DR N-PSDB; AAH90731.
 DR
 PT Nucleic acids encoding conserved essential genes involved in bacterial
 PT replication which are potential targets for the treatment of antibiotic
 PT resistant bacterial infections -
 XX
 XX Claim 27; Page 273; 380pp; English.
 CC The present invention relates to nucleic acids (AAH90701-AAH90918)
 CC encoding polypeptides (AAU01002-AAU0114), which are essential for the
 CC viability of a bacterial cell wall. The acronym CFE stands for "Conserved
 CC Expression", where CEG stands for "Conserved Essential Gene". The nucleic

XX Streptococcus pneumoniae.
OS
XX
XX WO200044885-A1.
XX
XX 03-AUG-2000
XX
XX 19-JAN-2000; 2000WO-US01131.
XX
XX 27-JAN-1999; 99US-0239052.
XX
XX (SMK) SMITHKLINE BEECHAM CORP.
XX
XX Holmes DJ, Mooney J, Zhong YF, Debouck C, Jaworski D, Wang M,
PI Warren RL, Kosmicka AL, McDevitt D, Ingraham KA, Chalker AF;
PI So CY, Wallis NG, Pearson SC;
XX
XX MPI: 2000-482971/42.
XX
XX N-PSDB: AAA74684.
XX
XX FabG polypeptide, isolated from Streptococcus pneumoniae, is used to
PT treat microbial diseases, identify agonists and antagonists for
PT treating microbial infections and to detect diseases associated with
PT microbial infections -
XX
XX
XX Claim 1; Page 3; 40pp; English.
XX
XX The present sequence is a FabG (2-oxoacyl-acyl carrier protein
CC reductase) polypeptide. A full length FabG gene was isolated from a
CC Streptococcus pneumoniae 0100993 DNA library in E. coli. FabG
CC polynucleotides and polypeptides are used for detection and treatment of
CC microbial diseases. They may also be used to identify antagonists and
CC agonists which can then be used to treat microbial diseases. Compounds
CC that interfere with the initial physical interaction between a pathogen
CC and a host have been identified. The compounds are able to prevent the
CC adhesion of bacteria to mammalian extracellular proteins in wounds,
CC prevent adhesion between mammalian extracellular proteins and bacterial
CC FabG proteins which mediate tissue damage and/or to block normal
CC progression of pathogenesis in infections mediated by implantation of
CC in-dwelling devices or other surgical techniques. The FabG
CC polypeptides, polynucleotides, antagonists and agonists are especially
CC useful in the treatment of Helicobacter pylori infection. They may be
CC used to decrease H. pylori-induced cancers and to prevent, inhibit
CC and/or cure gastric ulcers and gastritis.
XX
XX Sequence 243 AA;
SQ
Query Match 25.0%; Score 326.5; DB 21; Length 243;
Best Local Similarity 35.1%; Pred. No. 5e-23;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

AAU37767
ID AAU37767 standard; Protein; 243 AA.
XX
XX
XX AAU37767;
AC
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX Streptococcus pneumoniae cellular proliferation protein #196.
DE
XX
XX Antisense: prokaryotic cellular proliferation protein;
KW antibiotic; antibacterial; drug design.
XX
XX Streptococcus pneumoniae.
OS
XX
XX WO200170955-A2.
XX
XX 27-SEP-2001.
XX
XX
XX 21-MAR-2001; 2001WO-US09180.
XX
XX 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX MPI: 2001-611495/70.
XX
XX N-PSDB: AAS55626.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX
XX Example 3; Seq ID No 13360; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX
XX Sequence 243 AA;
SQ
Query Match 25.0%; Score 326.5; DB 22; Length 243;
Best Local Similarity 35.1%; Pred. No. 5e-23;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

XX New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -
Claim 1; Page 3542; 4525bp; English.

CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/SBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and anti-inflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.

SQ Sequence 243 AA:

Query Match 26.9%; Score 351; DB 23; Length 243;
Best Local Similarity 35.4%; Pred. No. 2,3e-25;
Matches 92; Conservative 42; Mismatches 100; Indels 26; Gaps 6

OY 8 VGLGIVAVITGGASGSLGTAERLVQGQASAVLLDIPNSGGEQAOKKT-----GNNCVF 60
Db 3 IKGNI-FITSGTGTGIGLAAHQFASILEANITYL-----NGRSALISEELVASFTDYGVTVVY 56
OY 61 APADVISEKDVCFALALAKGKRGARDVANCAGIAVASKTYNLKKQTHTLEDFOFLDV 120
Db 57 ISGDVEEASARKRVNEALEISGISIDLYVNNAGIT-----NDKLMLKMEDDFERYVLKI 110
OY 121 NLMGTTNTRLVAGEENGONEPDQGRGVIIINTASVAAEFGQVGQAAYSASKGIYGMTL 180
Db 111 NLGFAENMQSYLV-----KPMIKARQCAIINVSVMGLTGNIQNAVYAASKGMIGFTK 164
OY 181 PIARDAPIGIRWTFAPGLFCTPLITSPEKVCNFILASGYVPFSRIGDAEYAHVQAI 240
Db 165 SVAREEAARNICNALAPFISIDMTGYLPKMEQQLISQILPM-KRI GKRAQEVAAHLASF 223
OY 241 IENPFINGEYIRLDGAIRMQ 260
Db 224 VEODYITGVIAIDGGMTNQ 243

RESULT 8

ID AAM80670 standard; Protein: 243 AA.

XX AAM80670;

DE 24-DEC-1998 (first entry)

XX S. pneumoniae fatty acid biosynthesis protein.

KM Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip;
KM virulence; antibody; infection; detection; treatment; hypothetical;
XX cell wall biosynthetic, external target; minimal gene set protein.

OS Streptococcus pneumoniae.

PN WO9826072-A1.

DD 18-JUN-1998.

PF , 09-DEC-1997; 97WO-US25278.

XX 13-DEC-1996; 96US-0036281.
PR
PA (ELIL) LILLY & CO ELI.
XX
PI Baltz RH, Burgett SG, Dehoff BS, Hoskins JR, Jaskunas SR;
PI Mills BJ, Norris PH, Peery RB, Rocky PK, Rostock PR;
PI Sketard PJ, Smith MC, Solenberg PJ, Treadway PJ;
PI Young Bellido ML;
DR WPI, 1998-348529/30.
XX
XX Streptococcus pneumoniae nucleic acid sequences - used in DNA chips
PT for evaluating gene expression, and identification of virulence
PT genes
XX
PS Claim 3; Page 270; 333pp; English.
XX
CC This sequence represents a S. pneumoniae fatty acid biosynthesis
CC protein. The invention provides DNA sequences (AAV65201 to AAV65304)
CC from the Streptococcus pneumoniae genome and corresponding protein
CC sequences (AAH80605 to AAH80728). The protein sequences are classified as
CC hypothetical, cell wall biosynthetic, external target, or minimal gene
CC set proteins. A recombinant host containing a vector comprising any of
CC the above nucleic acids can be used for the recombinant expression of the
CC proteins. The invention also provides a DNA chip having arrayed on it at
CC least 15 base pair fragment of any one or more of these DNA sequences.
CC The DNA chip can be used methods for evaluating gene expression in S.
CC pneumoniae and for identifying virulence genes in S. pneumoniae.
CC Antibodies that selectively bind to the above proteins or peptide
CC fragments can be used to treat S. pneumoniae infection. The antibodies
CC can also be used to detect S. pneumoniae cells.
SQ
Sequence 243 AA:

Query Match 25.0%; Score 326.5; DB 19; Length 243;
Best Local Similarity 35.1%; Pred. No. 5e-23;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

15 ITGASGIGLTAETRLYGQASAVLLDLPNSGGF-----AQAKKLGNNCYFAPADVTSE 68
||| : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 10 ITGSSRGIGLIANHFAQAGANIVL----NSRGAISELLAEFSNYGIKVPISGDVSDF 65
||| : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 69 KDVCATALLAKGKGRVDVAANCAGIAVASRTYNLKKGOTHTLEDFOVLDPVNLMGTFFNV 128
||| : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 66 ADARKMDIQALAEIGSVADVLYNNGI--TQPTIMMKM-----TEADFEXVLKNLTGFANNM 119
||| : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 129 IRLVAGEGNEDPDGGGRRGYIINTASYAAFEQGVQCAIYSASKGIGVMPLPIARDLAP 188
||| : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 120 IQSYLV-----KPMKAREGAILINSSVYGLMGINGQANYASRGLIGFTKSVAREEVS 173
||| : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 189 IGIRMTIAPGLFGEPILTSLPEKYCNFLASCVPSPSLGPDAEYAHLYQAIIENPFLNG 248
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 174 ENIRRNVIAPGMIESDMTAILSDRKKEITLQIPH-KESGQALEQYADLTIVLLAQGDVLTG 232
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 249 EYIRLDGAIKM 259
||| : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 233 QVIALDGGLSM 243

RESULT 9
ID AAB15706
AAAB15706 standard: Protein; 243 AA.

XX AC AAB15706;
XX
DT 07-DEC-2000 (first entry)
XX
XX Streptococcus pneumoniae Fabg polypeptide.
KW Streptococcus pneumoniae; Fabg; 3-oxoacyl-acyl carrier protein reductase;
antibacterial; cytostatic; anticancer; cancer; gastric ulcer; gastritis;
Helicobacter pylori infection; microbial infection.

Query	Match	Similarity	Score	DB	Length
Best Local Similarity	55.5%	Pred. No. 4,9e-55;			
Matches	141;	Conservative	35;	Mismatches	69;
				Indels	9;
				Gaps	3
QY	8	VKGLVAVITGGASGLTAERTLVGQASAVLLDLPSNGSGAOKKLGNNCYEPADVTS	67		
Db	143	IEGRVFTVYTGAAASGLGASARMLAAGAKVTLADL-----AEPKDAPESAVHAACDVTD	196		
QY	68	ENVOFALALAAKGERVDVNAANCAGIVASKTNTNKKGHTLEDQORLVDTNLTGTFN	127		
Db	197	ATPAQAQALMALDTRGRLDGLVNCAGIAPAEEM--LGHDGPHGLDSRRAVTTNLIGSFN	254		
QY	128	VILTVAGENGQNEPDGQGGVYIINTASVAAFEGQVQGAAYASAKSGIVGMLPIARDIA	187		
Db	255	MARLAAEAMARNPEVR--GERGVYNTASIAADQDQIGQVAYAAKAGVAGMTLPMARDIA	313		
QY	188	PIGIRWMTAPGLFGFPLTSLPEVCNPLASQVPEPBRGDPAEVAHLVQALITENPFLN	247		
Db	314	RHGIRWMTAPGLFGFPLTSLPEVCNPLASQVPEPBRGDPAEVAHLVQALITENPFLN	373		
QY	248	GEVIRLDGARMP 261			
Db	374	GEVIRLDGARMP 387			
RESULT 6					
ABP28011					
ID	ABP28011	standard; Protein; 244 AA.			
AC	ABP28011;				
XX	02-JUL-2002	(first entry)			
XX	Streptococcus polypeptide SEQ ID NO 5198.				
XX	Streptococcus GAS; GAS; group B streptococcus; Streptococcus agalactiae;				
XX	group A streptococcus; Streptococcus pyogenes; antibacterial;				
XX	antiflammatory; infection; vaccine; meningitis; gene therapy.				
OS	Streptococcus agalactiae.				
XX	WO200234771-A2.				
XX	02-MAY-2002;				
XX	29-OCT-2001; 2001WO-GH04789.				
XX	27-OCT-2000; 2000GB-0026333.				
XX	24-NOV-2000; 2000GB-0028727.				
XX	07-MAR-2001; 2001GB-0005640.				
XX	(CHIR-) CHIRON SPA.				
XX	(GENO-) INST GENOMIC RES.				
XX	Telford J, Maignani V, Margarit Ros YI, Grandi G, Fraser C;				
XX	Tectelin H;				
XX	WPI; 2002-352536/38.				
XX	DR N-PSDB; ABN68642.				
XX	New Streptococcus protein for the treatment or prevention of infection				
XX	or disease caused by Streptococcus bacteria, such as meningitis, and				
XX	for detecting a compound that binds to the protein -				
XX	Claim 1; Page 3863; 4525pp; English.				
XX	The invention relates to a protein (ABP25413-ABP30895) from group B				
XX	Streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS				
XX	(Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in				
XX	the specification. The proteins have antibacterial and antiinflammatory				
XX	activity. (1), nucleic acids encoding (1), ABN6044-ABN71526 and				
XX	antibodies that bind (1) are used in the manufacture of medicaments for				

[illegible]

CC (see AAX00611 for described uses).

XX Sequence 227 AA:

Query Match 87.9%; Score 1146; DB 20; Length 227;

Best Local Similarity 100.0%; Pred. No. 2.5e-101;

Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 ASAVILDLPSNGGEAOKKRIKNNCVAPADVTSEKVCYRLALAKKRFGRVAVAVACAI 94
 DB 1 ASAVILDLPSNGGEAOKKRIKNNCVAPADVTSEKVCYRLALAKKRFGRVAVAVACAI 60
 QY 95 AVASKTYNLKKGQTHLEDFQRYLDVNLKMGTFNVIRLVAGEMQNEPDGQGRGYIINTA 154
 DB 61 AVASKTYNLKKGQTHLEDFQRYLDVNLKMGTFNVIRLVAGEMQNEPDGQGRGYIINTA 120
 QY 155 SVAAFEGQVQAAYASASKGIVGNTLPFIARDLPFGIRVWTTPAGLFGPILTSLEPKYC 214
 DB 121 SVAAFEGQVQAAYASASKGIVGNTLPFIARDLPFGIRVWTTPAGLFGPILTSLEPKYC 180
 QY 215 NFLASQVFPFSPRLGDPAEVAHLVQALIEFPFLNGEVRILDGAIKMP 261
 DB 181 NFLASQVFPFSPRLGDPAEVAHLVQALIEFPFLNGEVRILDGAIKMP 227

RESULT 4
 ABB62988 ID ABB62988 standard; Protein; 255 AA.

XX AC ABB62988;

XX XX 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 15756.

KM Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

OS Drosophila melanogaster.

XX XX WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX XX (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

XX XX WPI; 2001-655860/75.

DR N-PSDB; ABL07091.

PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

XX XX Disclosure: SEQ ID NO 15756; 21pp + Sequence Listing; English.

PS The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA

CC sequences (AB10840-AB116175) and the encoded proteins

CC (AB57737-AB572072).

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 255 AA:

Query Match 69.6%; Score 908; DB 22; Length 255;

Best Local Similarity 68.9%; Pred. No. 1.6e-78;

Matches 175; Conservative 29; Mismatches 50; Indels 0; Gaps 0;

QY 8 VKGLVAVITGGASGGLTAERLYQGASAVLLDLPNSGGEAOKKRIKNNCVAPADVT 67
 DB 2 IKNAVSLVTGGASGIGRAIETRIAKQASVILLADLPSSKGNEVAKELCDKVFVPDVT 61
 QY 68 EKDVOTALALAKGFRVDVAVNCAGIAVASKTYNLKKGQTHLEDFQRYLDVNLKMGTFN 127
 DB 62 EKDVSAALQTAADKFGRLDITVNCAGIATAVKTENFNKVAHRLDEFQRYININTVGTEN 121
 QY 128 VRIIVAGEMQNEPDGQGRGYIINTASVAAFEGQVQAAYASASKGIVGNTLPFIARDLA 187
 DB 122 VRIIVAGEMQNEPDGQGRGYIINTASVAAFEGQVQAAYASASKGIVGNTLPFIARDLS 181
 QY 188 PIGIRVMTIAPGLFGPILTSLEPKVCNFTLASQVFPFSPRLGDPAEVAHLVQALIEFP 247
 DB 182 TGGIRCTIAPGLFGPILTSLEPKVCNFTLASQVFPFSPRLGDPAEVAHLVQALIEFP 241
 QY 248 GEVIRIDGAIKMP 261
 DB 242 GEVIRIDGAIKMP 255

RESULT 5

AAM06513 ID AAM06513 standard; Protein; 388 AA.

XX AC AAM06513;

XX XX 08-MAR-1997 (first entry)

DE Flavobacterium ORF-5 gene product.

KM Carotenoid; lycopene; beta-carotene; echinenone; canthaxanthin;

KM zeaxanthin; adonixanthin; astaxanthin.

OS Flavobacterium sp. R1534 WT (ATCC 21568).

XX XX EP747483-A2.

PN 11-DEC-1996.

PD 29-MAY-1996; 96EP-0108556.

PF 09-JUN-1995; 95EP-0108888.

PR (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX XX Hohmann H, Pasamontes L, Tessier M, Van Loon A;

XX XX WPI; 1997-023160/03.

DR N-PSDB; AAT45143.

PT Flavobacterium gene sequences encoding carotenoid biosynthesis

PT enzymes - for the production of carotenoid(s), useful in foods and

XX XX animal feeds

PS Example 2; Fig 7; 80pp; English.

CC A polypeptide (AAM06513) showing approx. 30% homology to

CC streptomycete polyketide synthases was identified as the product

CC of ORF-5 from a carotenoid gene cluster (see also AAT45143) of

CC Flavobacterium sp. R1534. 5 Other open reading frames (see also

CC AAM06515-18 and AAM0871) and can be used to produce carotenoids in

CC transformed host cells.

XX Sequence 388 AA;

Query Match	88.1%	Score 1149	DB 21	Length 260
Best Local Similarity	88.0%	Pred. No. 1.5e-101		
Matches 227	Conservative 18	Mismatches 13	Indels 0	Gaps 0
DB	4	AVRSKGLVAVITGASGIGLATAARLYGCGASAVLLDPNPGSGGAOKKGNVCFAFA	63	
DB	3	AVRSKGLVAVITGASGIGLATAARLYGCGATVALLDPDSEGGGAOKKLBSCIFFA	62	
QY	64	DVTSKEDVQFATALAKRGFRGVAVVNCAGIYVASKRTLLKGGQHTLLEDFORVLDVNL	123	
DB	63	NVTSKEIQALITLAKKEKFRIDVAVNCAGIYVAKITVYHQKKNKHTLLEDFORVAVNL	122	
QY	124	GFFNVIRIVAGMGONENPDGQGRVITNTASVAFEGVGGVGAASASKGIYGMTLPIA	183	
DB	123	GFFNVIRIVAGMGONENPDGQGRVITNTASVAFEGVGGVGAASASKGIYGMTLPIA	182	
QY	184	RDIAPIGIRVMTIAGLFGTPLLTSIPKVCNFIASQVFPFRLGDPADYAHVQAIIEN	243	
DB	183	RDIAPIGIRVMTIAGLFGTPLLTSIPKVCNFIASQVFPFRLGDPADYAHVQAIIEN	242	
QY	244	PLNGEVIRLDGAIKMP 261		
DB	243	PLNGEVIRLDGAIKMP 260		

XX	25-MAR-1999	(first entry)	
DT			
XX		Fragment of human secreted protein encoded by gene 8.	
DE			
XX			
KW	Human; secreted protein; fusion protein; gene therapy; protein therapy;		
KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;		
KW	developmental abnormality; foetal deficiency; blood; allergy; renal;		
KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;		
KW	inflammation; ischaemic shock; Alzheimer's disease; stenosis; AIDS;		
KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;		
KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;		
KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.		
XX			
OS	Homo sapiens.		
XX			
PN	W09842738-A1.		
XX			
PD	01-OCT-1998.		
FE			
XX	19-MAR-1998; 98WC-US05311.		
XX			
PR	30-MAY-1997; 97US-0050937.		
PR	21-MAR-1997; 97US-0041276.		
PR	21-MAR-1997; 97US-0041277.		
PR	21-MAR-1997; 97US-0041281.		
PR	21-MAR-1997; 97US-0042344.		
PR	30-MAY-1997; 97US-0048069.		
PR	30-MAY-1997; 97US-0048094.		
PR	30-MAY-1997; 97US-0048095.		
PR	30-MAY-1997; 97US-0048096.		
PR	30-MAY-1997; 97US-0048131.		
PR	30-MAY-1997; 97US-0048135.		
PR	30-MAY-1997; 97US-0048154.		
PR	30-MAY-1997; 97US-0048160.		
PR	30-MAY-1997; 97US-0048186.		
PR	30-MAY-1997; 97US-0048187.		
PR	30-MAY-1997; 97US-0048188.		
PR	30-MAY-1997; 97US-0048350.		
PR	30-MAY-1997; 97US-0048351.		
PR	30-MAY-1997; 97US-0048352.		
PR	30-MAY-1997; 97US-0048355.		
PR	05-AUG-1997; 97US-0054804.		
PA			
XX	(HUMA-) HUMAN GENOME SCI INC.		
XX			
PI	Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA;		
PI	Greene JM, Hu JS, Laflaur DW, Moore PA, Ni J, Olsen HS;		
PI	Rosen CA, Ruben SM, Shi Y, Young P;		
XX			
DR	WPI; 1999-070066/06.		
DR	N-PSDB; AAX00618.		
XX			
PT	New isolated human genes and the secreted polypeptides they encode -		
PT	useful for diagnosis and treatment of e.g. cancers, neurological		
PT	disorders, immune diseases, inflammation or blood disorders		
XX			
PS	Disclosure; Page 11; 385pp; English.		
XX			
CC	This sequence represents a fragment of a secreted human protein encoded		
CC	by the nucleic acid molecule detailed in the descriptor line. The gene		
CC	can be used to generate fusion proteins by linking to the gene to a		
CC	human immunoglobulin Fc portion (e.g. AAX00602) for increasing the		
CC	stability of the fused protein as compared to their fragments (nucleic		
CC	acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)		
CC	which are useful for preventing, treating or ameliorating medical		
CC	conditions e.g. by protein or gene therapy. Also, pathological		
CC	conditions can be diagnosed by determining the amount of the new		
CC	polypeptides in a sample or by determining the presence of mutations in		
CC	the new polynucleotides. Specific uses are described for each of the 87		
CC	polynucleotides based on which tissues they are most highly expressed in		

84	265.5	20.4	246	22	AAE02195	S. aureus NADPH-de
85	265.5	20.4	268	22	ABE52552	Escherichia coli p
86	264	20.2	247	16	AAE62921	Mycobacterium bovi
87	264	20.2	247	16	AAE63899	M. Bovis p55 ORF1
88	264	20.2	247	18	AAW40809	M. Bovis p55 opeto
89	264	20.2	276	21	AAV54416	Secoisolaricidresin
90	264	20.2	276	23	AAO21494	Secoisolaricidresin
91	263	20.1	251	13	AAE27556	NAD affinity gluco
92	262.5	20.1	252	23	AAO16940	Recombinant enzyme
93	261	20.0	272	21	AAE10740	B. megaterium gluc
94	261	20.0	277	21	AAV54413	Secoisolaricidresin
95	261	20.0	340	21	AAE10741	H. gillii/anti/B. me
96	260.5	20.0	273	21	AAV54414	Secoisolaricidresin
97	260	19.9	243	23	ABE54107	Lactococcus lactis
98	259	19.9	253	22	AAU36249	Pseudomonas aerugi
99	258	19.8	283	21	AAE31552	Arabidopsis thalia
100	258	19.8	283	23	ABE92823	Herbicideally activ

ALIGNMENTS

RESULT 1

AAW71471 standard; Protein; 261 AA.

AAW71471;
16-DEC-1998 (first entry)
ERAB protein.

Endoplasmic reticulum associated amyloid-beta peptide binding protein;
ERAB protein; amyloid-beta peptide inhibitor; demyelinating disease;
neurodegenerative disorder; therapy; Alzheimer's disease; schizophrenia;
Down's syndrome; Parkinson's disease; Huntington's disease;
multiple sclerosis.

Homo sapiens.

MO9840484-A1.

17-SEP-1998.

12-MAR-1998; 98WO-US04915.

12-MAR-1997; 97US-0815225.

(UYCO) UNIV COLUMBIA NEW YORK.

Stern DM, Yan SD;

WPI: 1998-531524/45.

N-PSSB; AAV60576.

Endoplasmic reticulum associated amyloid-beta peptide binding
protein - inhibitors of which can be used to treat neurodegenerative
disorders

Claim 2; Fig 1D; 53pp; English.

This sequence is the endoplasmic reticulum associated amyloid-beta
peptide binding (ERAB) protein of the invention. The protein can be used
in a method for evaluating the ability of an agent to inhibit binding of
ERAB polypeptide to amyloid-beta peptide comprising: (a) incubating the
ERAB polypeptide, the agent and amyloid-beta peptide under binding
conditions; (b) determining the amount of amyloid-beta peptide bound to
ERAB polypeptide; (c) comparison of the amount of binding with results
from a control using no agent, so determining inhibition ability of the
agent. The inhibitors identified by the method can be used to treat a
neurodegenerative condition by administration of an agent that inhibits
binding of an ERAB polypeptide to amyloid-beta peptide, particularly,

disease, Huntington's disease, schizophrenia, a demyelinating disease, or
multiple sclerosis. The inhibitors can also be used to treat other
neurodegenerative conditions including those associated with ageing,
dentatorubral and pallidolysian atrophy, Machado-Joseph disease,
muscular dystrophy, senility, spinocerebellar ataxia type I, spinobulbar
muscular atrophy, stroke, and trauma.

SQ Sequence 261 AA;

Query Match 99.6%; Score 1299; DB 19; Length 261;
Best Local Similarity 99.6%; Pred. No 7 3e-116;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MAAAYSVKGLVAVITGASGLGATPAERLVGGASAVLLDLPNSGGEAAKKGNNVF	60
DB	1	MAAACRSVKGLVAVITGASGLGATPAERLVGGASAVLLDLPNSGGEAAKKGNNVF	60
QY	61	APADVTSEKDVOTATLAKKFGFRVDVAVNACAGIAVASKTYNKKQTHLEDFORVLDV	120
DB	61	APADVTSEKDVOTATLAKKFGFRVDVAVNACAGIAVASKTYNKKQTHLEDFORVLDV	120
QY	121	NLMGTENVIRLVAGEMQNEPDGOGGVIIINTASVAEEGGVGAAYASAKSGIVGML	180
DB	121	NLMGTENVIRLVAGEMQNEPDGOGGVIIINTASVAEEGGVGAAYASAKSGIVGML	180
QY	181	PIARDLAPIGIRWTAPGIFGTPLTSLPEKVCNPLASGVPPSRFGPAEYAHVQAI	240
DB	181	PIARDLAPIGIRWTAPGIFGTPLTSLPEKVCNPLASGVPPSRFGPAEYAHVQAI	240
QY	241	IENPFLNGEYIRLDGAIKMP	261
DB	241	IENPFLNGEYIRLDGAIKMP	261

RESULT 2

AAV32239 standard; Protein; 260 AA.

AAV32239;

15-FEB-2000 (first entry)

Alzheimer-associated beta-amyloid binding protein (ERAB).

Alzheimer-associated beta-amyloid binding protein; ERAB; mouse;

Leydig cell; differential display RT-PCR; DDRT-PCR;

short chain alcohol dehydrogenase; SCAD; testis; marker;

Mus musculus.

Location/Qualifiers

Region "beta sheet region A"

Region "alpha helix region A"

Region "beta sheet region B"

Region "alpha helix region B"

Region "beta sheet region C"

Region "alpha helix region C"

Region "beta sheet region D"

Region "alpha helix region D"

Region "beta sheet region E"

Region "SCAD motif"

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 14:19:21 ; Search time 39.6667 Seconds
(without alignments)
876.767 Million cell updates/sec

Title: US-09-931-186-4
Perfect score: 1304
Sequence: 1 MAARVSVKGLAVITGSAS.....ENPLNGEVRIDDAIRIMQP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1960.DAT:*
2: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1961.DAT:*
3: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1962.DAT:*
4: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1963.DAT:*
5: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1964.DAT:*
6: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1965.DAT:*
7: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1966.DAT:*
8: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1967.DAT:*
9: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1968.DAT:*
10: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1969.DAT:*
11: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1970.DAT:*
12: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1971.DAT:*
13: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1972.DAT:*
14: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1973.DAT:*
15: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1974.DAT:*
16: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1975.DAT:*
17: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1976.DAT:*
18: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1977.DAT:*
19: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1978.DAT:*
20: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1979.DAT:*
21: /SID22/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SID22/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SID22/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1299	99.6	261	19	AAW71471
2	1149	88.1	260	21	AAV32239
3	1146	87.9	227	20	AAW67934
4	908	69.6	255	22	ABB62988
5	664.5	51.0	388	18	AAW06513
6	361.5	27.7	244	23	ABP28011
7	351	26.9	243	23	ABP27345
8	326.5	25.0	243	21	AAW80670
9	326.5	25.0	243	21	AAW15706
10	326.5	25.0	243	22	AAU37767

11	326.5	25.0	243	22	AAU37988
12	325.5	25.0	243	22	AAW01032
13	324.5	24.9	243	23	ABW4087
14	318.5	24.4	245	22	AAU35328
15	314	24.1	237	22	AAW50255
16	313.5	24.0	241	22	AAW63937
17	312	23.9	237	22	AAU28156
18	312	23.9	237	22	AAW19928
19	312	23.9	257	22	AAU28344
20	310.5	23.8	248	21	AAV54422
21	303.5	23.3	247	23	ABW48892
22	301.5	23.1	247	22	AAU28296
23	301	23.1	247	21	AAV5746
24	296	22.7	315	17	AAW9323
25	296	22.7	315	17	AAW9322
26	295	22.6	263	23	ABP39667
27	294	22.5	262	22	AAW63032
28	293.5	22.5	267	22	AAW47459
29	292.5	22.4	262	22	AAW6337
30	291.5	22.4	270	20	AAV41761
31	291.5	22.4	270	21	AAW44317
32	291.5	22.4	270	21	AAW44056
33	291.5	22.4	270	22	AAW28108
34	291.5	22.4	279	22	AAU18296
35	289.5	22.2	244	21	AAV54421
36	289.5	22.2	244	22	AAU34533
37	288.5	22.1	246	12	AAU10974
38	288.5	22.1	262	21	AAV4578
39	288	22.1	263	10	AAU38499
40	287.5	22.0	246	10	AAW4157
41	287.5	22.0	246	14	AAW32192
42	287.5	22.0	246	20	AAV3310
43	287.5	22.0	246	21	AAV54423
44	287.5	22.0	246	22	AAW1981
45	287.5	22.0	270	21	AAW42558
46	287.5	22.0	277	21	AAV54415
47	287.5	22.0	303	23	ABW2654
48	287.5	22.0	329	16	AAW1324
49	285.5	21.7	253	23	ABW54214
50	282.5	21.7	273	10	AAW94155
51	282	21.6	280	23	ABW92449
52	280.5	21.5	254	22	AAW49773
53	280.5	21.5	306	22	AAW81644
54	279.5	21.4	241	12	AAW10679
55	278.5	21.4	242	22	AAU59290
56	278.5	21.4	274	23	ABP39586
57	278	21.4	244	22	AAW61318
58	276	21.2	258	22	AAW92682
59	276	21.2	258	22	AAW79361
60	276	21.2	285	22	AAW34668
61	275	21.1	246	14	AAW47461
62	274.5	21.1	254	22	AAW47522
63	274.5	21.1	269	23	ABW52448
64	274	21.0	206	23	AAU99345
65	273.5	21.0	249	23	ABP39980
66	273.5	21.0	272	22	AAU37095
67	273	20.9	202	23	AAU77210
68	272.5	20.9	286	22	AAU62657
69	271.5	20.8	251	22	AAU34193
70	270.5	20.7	267	21	AAW35505
71	270.5	20.7	308	21	AAW35504
72	269.5	20.7	246	21	AAW15707
73	269.5	20.7	246	22	AAU33965
74	269.5	20.7	246	22	AAU36530
75	269.5	20.7	246	22	AAU37210
76	269.5	20.7	246	22	AAU37507
77	269	20.6	231	22	ABP39552
78	268.5	20.6	248	20	AAW16959
79	268	20.6	186	19	AAW38474
80	267.5	20.5	166	21	AAW32509
81	267.5	20.5	336	16	AAW06468
82	266.5	20.4	242	22	AAU53381
83	266	20.4	254	23	ABW48207

Streptococcus pneu
CFE 35 protei
Lactococcus lactis
Enterococcus faeca
Human dehydrogenas
Putative P. abyssal
Novel human secret
Human oxireducta
Novel human secret
Amino acid sequenc
Listeria monocytog
Novel human secret
Bacillus megaterium
Rape leaf beta-ket
Staphylococcus epi
S. epidermidis ope
Levodione reductas
G. suboxydans DSM
Human PRO474 prote
Human PRO474 (UNO5
Human PRO474 prote
Novel human secret
Human endocrine po
Amino acid sequenc
E. coli cellular p
Acetoacetyl COA re
Xylitol dehydrogen
Salmonella typhi c
Acetyl COA reducta
Sequence encoded b
Acetoacetyl COA re
Amino acid sequenc
Ralstonia eutropha
Human ORFX CRP2322
Secoisolaricresin
Herbicidally activ
Acetyl COA reducta
Lactococcus lactis
Acetyl COA reducta
Herbicidally activ
Protein with acetyl
S. epidermidis ope
Acetoacetyl COA re
Propionibacterium
Staphylococcus epi
Human AFP protein
C glutamicum prote
Corynebacterium g1
E. coli cellular p
Acetoacetyl COA re
(R)-2-octanol dehy
Herbicidally activ
Short-chain dehydr
Staphylococcus epi
Staphylococcus aut
Staphylococcus aut
Staphylococcus aut
Staphylococcus epi
Staphylococcus epi
Chlamydia trachoma
S. pneumoniae 3-ox
Human OXRE-6. Hom
Maize T82 sequence
Haemophilus influe
Listeria monocytog

Thu Jun 26 06:55:07 2003

us-09-931-186-4.rai

Page 12

Search completed: June 23, 2003, 14:35:39
Job time : 13.1667 secs

Thu Jun 26 06:55:07 2003

us-09-931-186-4.ra1

Page 11

REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 270:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6348328e
US-08-856-207A-270

Query Match 20.6%; Score 268; DB 4; Length 186;
Best Local Similarity 38.7%; Pred. No. 7,7e-22;
Matches 74; Conservative 23; Mismatches 72; Indels 22; Gaps 5;

QY 15 ITGASGGLATAEERLVGOGASAVLLDLPNSGGE-----AQAKLNNCFAPADVTSE 68
DB 10 ITGSSRGIGLAIHKEFAQGANIVL-----NSRGALSEELLAEFSNYGKRVVPGSDVDF 65
QY 69 KVVQALALAKKGFGRVDVAVNCAGIYASAKTYNKKGQTHLEDFQVLDVNLMTGTVN 128
DB 66 AAKKRIIDQALIELGSVDVLYNNAGI---TQDTLMKMK---TEADFEKVLKYNLGTAFNM 119
QY 129 IRLVAGEMQNEPDGQGRGVITNTASVAEFEGVGOAAYSASKGIYGMPLPIARDLAP 188
DB 120 TQSVL-----KPMKAREGAIINMSYVGLMGNIGQANTYASKAGLIGETKSVAREVAS 173
QY 189 IGRVMTIAPG 199
DB 174 RNIIRVNIAPG 184

RESULT 24
US-08-440-856A-3
Sequence 3, Application US/08440856A
Patent No. 5750873
GENERAL INFORMATION:
APPLICANT: DELAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
US-08-440-856A-3

Query Match 20.5%; Score 267.5; DB 1; Length 337;
Best Local Similarity 30.9%; Pred. No. 2,2e-21;
Matches 88; Conservative 44; Mismatches 112; Indels 41; Gaps 6;

QY 6 RSVKGLVAVITGASGGLATAEERLVGOGASAVLLDLPNSGGEAQAQKIGNNCFAPADY 65
DB 51 KRLDKYALVITGARGIGELIVLEFAKHGARGVYADIDDAAGBALASALGPQVSFEVCDV 110
QY 66 TSEKDVOTLALAKGR-GRVDVAVNAGIYASAKTYNKKGQTHLEDFQVLDVNLMTG 124
DB 111 SVEDDVRAVDWMLSRGRLDYCNNAV-LGRQTPAARSILSTFPAEEDRVLRVNALG 169
QY 125 TENVIRLVAGEMQNEPDGQGRGVITNTASVAEFEGVGOAAYSASKGIYGMPLPIAR 184
DB 170 AALGMKHAARAPR-----RAGSIYASVAVALGGLGPHAYTSKHAIVGLTKNPAAC 223
QY 185 DLAPIGIRVMTIAPGLTLP-----TSLE-----EX 212
DB 224 ELRAHGVAVNCVSFEVATPMLINAWQGHDDATADRDLDLDLVTPSDQVEKME 283
QY 213 VCNFLASQVFPFPRSLGPAEYAHVQAIIENPFLNGEVIRLDGAI 257
DB 284 VVRGLATLKGTELRPRDIAE-AVLFLASDEARYISGHNLVVDGV 327

RESULT 25
US-09-504-358-14
Sequence 14, Application US/09504358
Patent No. 6365376
GENERAL INFORMATION:
APPLICANT: Rouviere, Pierre E.
APPLICANT: Brzostowicz, Patricia C.
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIA
FILE REFERENCE: BCI001 US NA
CURRENT FILING DATE: 2000-02-15
CURRENT APPLICATION NUMBER: US/09/504,358
EARLIER FILING DATE: 2000-12-02
EARLIER FILING DATE: 1999-February-19
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 256
TYPE: PRT
ORGANISM: Brevibacterium sp HCU
US-09-504-358-14

Query Match 20.4%; Score 266; DB 4; Length 256;
Best Local Similarity 30.9%; Pred. No. 2,1e-21;
Matches 82; Conservative 39; Mismatches 116; Indels 28; Gaps 8;

QY 10 GLVAVITGASGGLATAEERLVGOGASAVLLDLPNSGGEAQAQKL---GNNCFAPADY 66
DB 6 GRVAVITGASGGMGRIGSELASEGQAVAVDVMBEGRATADAIASGAVANWKLDVS 65
QY 67 SEKDVOYLALAKKGFGRVDVAVNAGIYASAKTYNKKGQTHLE--DFQVLDVNLMTG 124
DB 66 DESEVEIIVSDIAKRFGINVLYNNAGVTGADK-----PTHEDERDLDLVISVDVGK 118
QY 125 TENVIRLVAGEMQNEPDGQGRGVITNTASVAEFEGVGOAAYSASKGIYGMPLPIAR 184
DB 119 VEFMTKHCIPYKQ---AGG--GAIYVFAIYIGVSGDELTPHAAAGAVALLTKDAY 172
QY 185 DLAPIGIRVMTIAPGLTLPPLTSLPEK-----VCNFLASQVFPFRLDPAEY--AH 235
DB 173 TYGPENIRVNNVAPGTITLPVKEIGSRGPDLDGYTKLMGAKHPL-GRVGTPEVNAAT 231
QY 236 LVCAITENPFLNGEVIRLDGAIIRMO 260
DB 232 LFLASEBASFTIGAVLPYDGGITAO 256

Thu Jun 26 06:55:07 2003

us-09-931-186-4.ra1

Page 9

FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 67,695
FILING DATE: 29-JUN-1987
SEQ ID NO: 4
LENGTH: 273
5512669-4

Query Match 21.7%; Score 282.5; DB 6; Length 273;
Best Local Similarity 31.5%; Pred. No. 3.4e-23;
Matches 90; Conservative 42; Mismatches 91; Indels 63; Gaps 11;

QY 12 VAVITGGASGLATRAERLYVGOGASAVLLDLPNSGGEQAQKLGNNCYFA----- 63
DB 4 VALVTGSGRGID-----AISTALKAAQYKVAASYAGNDDAKPKAETGTAV 51
QY 64 ---DVTSEKDVOTALALAKGKRGVAVVNCAGIYVASKTYNLKKGQTH--TLEDFOHVL 118
DB 52 YKMDVSYIACVEGIAGIAKAEADLGPIDVLYNNAGIT-----KAMFHKMTPDQMNVI 103
QY 119 DVMNLTGTFNMTHPVYSGMDRSEGRIVNISSINGQKGMQANYSVSGMDRSPGRIVN 163
DB 104 NTNLTLGTFNMTHPVYSGMDRSEGRIVNISSINGQKGMQANYSVSGMDRSPGRIVN 163
QY 153 TASVAFEGOVGAAYASAKSGIVGNTLPIARDLAPIGRTVITAPGLFGLTSLPEK 212
DB 164 ISSINGQKGMQANYSVSGMDRSEGRIVNISSINGQKGMQANYSVSGMDRSPGRIVN 223
QY 213 VCN-FLASQVPEPSRLGDPAEYAHLY--QAITENPFLNGEVIRLDG 255
DB 224 VLERIIPQIPV-GRIGEPDEIARIYVELASDEAGITGTSISANG 268

RESULT 18
US-09-134-001C-4431
Sequence 4431, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134, 001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064, 964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055, 779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4431
LENGTH: 274
TYPE: PRT
ORGANISM: staphylococcus epidermidis
US-09-134-001C-4431

Query Match 21.4%; Score 278.5; DB 4; Length 274;
Best Local Similarity 31.7%; Pred. No. 9.6e-23;
Matches 85; Conservative 45; Mismatches 93; Indels 45; Gaps 8;

QY 12 VAVITGGASGLATRAERLYVGOGASAVLLDLP-----NSGGEQAQKLGNNCYF 60
DB 10 IAVITGASTIGOGASAVALLAIEGAHVLAIDISQLETVOSINDNGKATAYRV----- 63
QY 61 APADVSEKVOYALALAKGKRGVAVVNCAGIYVASKTYNLKKGQTH--TLEDFOHVL 118
DB 64 ---DISDDKOVKOFSEKIAOEFHGVYIFENAGVDGA-----GRHIEYPAVEVDKIM 113
QY 119 DVMNLTGTFNMTHPVYSGMDRSEGRIVNISSINGQKGMQANYSVSGMDRSPGRIVN 178
DB 114 AYDMRGFLVTKFL-----PLMKKGSSINTASFSQADLVRSYGNAKGVIN 166
QY 179 TLPIARDLAPIGRTVITAPGLFGLTSLPEKCNLASQ--VPEPSRLGDP 231
DB 167 TKSIATLEYGRENIRAAIALETPLVNDLACTSDEAGITREKQKWVTPJRLGTPD 226

QY 232 EYAHVVO--AITENPFLNGEVIRLDGAI 257
DB 227 EVGKLVAFIASDDSSFITGETIRIDGV 254

RESULT 19
US-09-134-001C-4825
Sequence 4825, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134, 001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064, 964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055, 779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4825
LENGTH: 249
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4825

Query Match 21.0%; Score 273.5; DB 4; Length 249;
Best Local Similarity 29.1%; Pred. No. 3e-22;
Matches 74; Conservative 54; Mismatches 105; Indels 21; Gaps 6;

QY 13 AVITGGASGLATRAERLYVGOGASAVLLDLPNSGGEQAQKLGNNCYFAPAVTS 67
DB 10 ALVTGASGIGRSTLQALAEIGYN-VAVNAGSKDKAEVVEELKAGVESFAIQANVAK 68
QY 68 EKDVOYOTALALAKGKRGVAVVNCAGIYVASKTYNLKKGQTH--TLEDFOHVLNMGTFN 127
DB 69 GDEVEMKEIVYSGQSVYDLVNNAGITKMDLMAKKE-----QEMDDVIDTMLKGVFN 122
QY 128 VYRLVAGMGNEPDGOGGVIIINTASVAFEGOVGAAYASAKSGIVGNTLPIARDL 187
DB 123 CIQKVTPLMLKQ-----RSGIILNLISIVGAMGPGQANTYATKAGVIGLTKTAARELA 176
QY 188 PIGIRVMTIAPGLFGLTSLPEKVCNFLASQVPEPSRLGDPAEYAHLYVAIEN--PF 245
DB 177 SRGITVNAVAPGFIVSDMTNLSDDLKQDMLEQIPL-KRFGEDPIDIANVAFIASDRAKY 235
QY 246 LMGVYIRLDGAI 259
DB 236 ITGQTIHVNGKTM 249

RESULT 20
US-09-238-481-2
Sequence 2, Application US/09238481
Patent No. 6110704
GENERAL INFORMATION:
APPLICANT: Huang, Jianzhong
APPLICANT: McDevitt, Damien
TITLE OF INVENTION: FabG
FILE REFERENCE: GM10192
CURRENT APPLICATION NUMBER: US/09/238, 481
CURRENT FILING DATE: 1999-01-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-238-481-2

Query Match 20.7%; Score 269.5; DB 3; Length 246;

APPLICATION NUMBER: 08/562,114
FILING DATE: 22-No. 6280997ember-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/375,962
FILING DATE: 20-January-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 10-June-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6280997man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5372.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
US-08-729-594A-13

Query Match 21.9%; Score 285.5; DB 4; Length 244;
Best Local Similarity 29.6%; Pred. No. 1.3e-23;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;
QY 9 KGLVAVITGGASGLGATLAEELVGGASAVLIDLPSNGGEQAOKLGNCCVFAADVTSE 68
DB 4 EKIALVTGASRGIRAIETLARGKVIGTATSENGAQAISDYLGNKGKGLMINTDP 63
QY 69 KDQVOTALAKKGFGRVDVAVACAGIAVASKTYNLKKGQHTLEDFOVLDVNLGTFNV 128
DB 64 ASIESVLEKTRAEFGEVDILVNNAGITRDNLKMKD-----EEMNDIIEFTNLSSVRL 117
QY 129 IRLVAGEQNEPDGQGVIIINTASVAFEQVQAAYASAKGIVGTLPIARDLAP 188
DB 118 SKAVRAMMK-----RHGRITIGSVGTMGNGQANVAAKAGIGFSKSLAREVAS 171
QY 189 IGRVMTIAPGLFGTPLTSLPEKVCNFLASQVPPSRGDPAEYAHVQ--AIIENPFL 246
DB 172 RGIIVNVVAPGFIETDMTRALSDQRAIGLAQVP-AGRLGGAQELIANVAFLASDEAYI 230
QY 247 NGEVIRLDGAIRM 259
DB 231 TGETLHVNGMYM 243

RESULT 16
US-08-937-993-13
Sequence 13, Application US/08937993
Patent No. 6399344
GENERAL INFORMATION:
APPLICANT: Eriksson, Ulf; Simon, Andreas; Romeit, Anna
TITLE OF INVENTION: ISOLATED PROTEINS HAVING CIS-R
TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,993

FILING DATE: September 26, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/729,594
FILING DATE: 11-October-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/562,114
FILING DATE: 22-No. 6399344ember-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/375,962
FILING DATE: 20-January-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 10-June-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6399344man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
US-08-937-993-13

Query Match 21.9%; Score 285.5; DB 4; Length 244;
Best Local Similarity 29.6%; Pred. No. 1.3e-23;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;
QY 9 KGLVAVITGGASGLGATLAEELVGGASAVLIDLPSNGGEQAOKLGNCCVFAADVTSE 68
DB 4 EKIALVTGASRGIRAIETLARGKVIGTATSENGAQAISDYLGNKGKGLMINTDP 63
QY 69 KDQVOTALAKKGFGRVDVAVACAGIAVASKTYNLKKGQHTLEDFOVLDVNLGTFNV 128
DB 64 ASIESVLEKTRAEFGEVDILVNNAGITRDNLKMKD-----EEMNDIIEFTNLSSVRL 117
QY 129 IRLVAGEQNEPDGQGVIIINTASVAFEQVQAAYASAKGIVGTLPIARDLAP 188
DB 118 SKAVRAMMK-----RHGRITIGSVGTMGNGQANVAAKAGIGFSKSLAREVAS 171
QY 189 IGRVMTIAPGLFGTPLTSLPEKVCNFLASQVPPSRGDPAEYAHVQ--AIIENPFL 246
DB 172 RGIIVNVVAPGFIETDMTRALSDQRAIGLAQVP-AGRLGGAQELIANVAFLASDEAYI 230
QY 247 NGEVIRLDGAIRM 259
DB 231 TGETLHVNGMYM 243

RESULT 17
5512669-4
Patent No. 5512669
APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
TITLE OF INVENTION: GENE ENCODING BACTERIAL ACETOACETYL-COA
REDUCTASE
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,667
FILING DATE: 29-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 124,570
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 944,488
FILING DATE: 03-NOV-1992
APPLICATION NUMBER: 566,535

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 6-October-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5372.1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]
NAME/KEY: reductase (FABG)
US-08-375-962B-13

Query Match 21.9%; Score 285.5; DB 1; Length 244;
Best Local Similarity 29.6%; Pred. No. 1.3e-23;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;

QY 9 KGLVAVITGGASGLGTAERLVGQASAVLLDLPNSGGGAQAKLGNVCYFAPADVTSE 68
D 4 EGRKIALVYGASRGGRALAEFLAARGKVGIGTATSENGAQAISDYLGANGKGLMNTDP 63
QY 69 KDVOFTALALAKGRTGVDVAVNAGIAVASKTYNLLKKQGTHTLDFQVRLDYNLMGTENV 128
D 64 ASIESVLEKIRAEFGVDILVNNAGITRDNLIMRKD-----EEMNDIETNLSVRL 117
QY 129 IRLVAGENGQNEPDGQGRGVITNTASVAEFGVQQAAYSASKGGIVGMLPIARDLAP 188
D 118 SKAVRAMKKR-----RHGRITITGSVGTMGNGGQANYAAAKGLIGFSKSLAREVAS 171
QY 189 IGIRVMTIAPGLFGTLLTSLPEKVCNFIASQVFPFSRLGDAEYAHVQ--AIENPFL 246
D 172 RGIITVNVAPGFIEIDMTALSDQGRGIIAQP-AGRLGGAQELIANNVAFLASDEAYI 230
QY 247 NGEVIRLDGAIRM 259
D 231 TGETLHVNGMYM 243

RESULT 14
US-08-562-114B-13
Sequence 13, Application US/08562114B
Patent No. 5972646
GENERAL INFORMATION:
APPLICANT: ERIKSSON ET AL.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH CODES FOR A
TITLE OF INVENTION: 32 KDA PROTEIN HAVING 11-CIS RETINOL HYDROGENASE
TITLE OF INVENTION: ACTIVITY, AND WHICH ASSOCIATES WITH P63, A
TITLE OF INVENTION: PORTION OF A RETINOL BINDING PROTEIN RECEPTOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect 5.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/562,114B
FILING DATE: 22-NO. 5972646ember-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/375,962
FILING DATE: 20-January-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kohli, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5372.2 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
NAME/KEY:
US-08-562-114B-13

Query Match 21.9%; Score 285.5; DB 2; Length 244;
Best Local Similarity 29.6%; Pred. No. 1.3e-23;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;

QY 9 KGLVAVITGGASGLGTAERLVGQASAVLLDLPNSGGGAQAKLGNVCYFAPADVTSE 68
D 4 EGRKIALVYGASRGGRALAEFLAARGKVGIGTATSENGAQAISDYLGANGKGLMNTDP 63
QY 69 KDVOFTALALAKGRTGVDVAVNAGIAVASKTYNLLKKQGTHTLDFQVRLDYNLMGTENV 128
D 64 ASIESVLEKIRAEFGVDILVNNAGITRDNLIMRKD-----EEMNDIETNLSVRL 117
QY 129 IRLVAGENGQNEPDGQGRGVITNTASVAEFGVQQAAYSASKGGIVGMLPIARDLAP 188
D 118 SKAVRAMKKR-----RHGRITITGSVGTMGNGGQANYAAAKGLIGFSKSLAREVAS 171
QY 189 IGIRVMTIAPGLFGTLLTSLPEKVCNFIASQVFPFSRLGDAEYAHVQ--AIENPFL 246
D 172 RGIITVNVAPGFIEIDMTALSDQGRGIIAQP-AGRLGGAQELIANNVAFLASDEAYI 230
QY 247 NGEVIRLDGAIRM 259
D 231 TGETLHVNGMYM 243

RESULT 15
US-08-729-594A-13
Sequence 13, Application US/08729594A
Patent No. 6280997
GENERAL INFORMATION:
APPLICANT: Eriksson, Ulf; Simon, Andreas; Romert, Anna
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH
TITLE OF INVENTION: CODES FOR A 32 KDA PROTEIN HAVING 11-CIS RETINOL DEHYDROGENASE
TITLE OF INVENTION: ACTIVITY, AND WHICH ASSOCIATES WITH P63, A PORTION OF A
TITLE OF INVENTION: RETINOL BINDING PROTEIN RECEPTOR
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,594A
FILING DATE: 11-October-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

Thu Jun 26 06:55:07 2003

us-09-931-186-4.ra1

Page 6

TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4512

Query Match 22.6%; Score 295; DB 4; Length 263;
Best Local Similarity 32.3%; Pred. No. 1.3e-24;
Matches 86; Conservative 42; Mismatches 104; Indels 34; Gaps 6;

12 VAVITGASGGLTAERLVGOGASAVLLDLPNSGGEAAKTL--GNNCEAPADYSE 68
11 VAVVVGAGOGIGLKTIERLEPDGYSTALVDENEAVAKESAKLSKEGGEAFAKADYSEN 70
69 KDVTALALAKGFRGVAVNCAGIYAVASKTYNLKKGOTHTLEDFORVLDVNMGTENV 128
71 DQVETLVNQVVEHGGDLVYNNAGLGPTPI-----ESVPEQFNQVGVNAGVFWG 124
129 IRLVAGEMQNEPDGQGVYIINTASVAFEGOVQAAVSASKGIVGMLPIARDLAP 188
125 IQAALIEQF-----DKLHGKGKIIINATSOQVGEANGLSYSTKFAVRGLTVAAARDLAE 179
189 IGRVMTIAPGLFGTPLTSLPEKVCNFIASQVPP-----SRLGDPAEYA 234
180 KNTVAFAPGIVETPEPMKGIAR-----LAENNOPMENGWKOFTDQIALKRLSKPEDEYA 235
235 HLVOAIT--ENPFLNGEVIRLDGATR 258
236 NVVSFLAGSDSDYITGTITIDGMR 261

RESULT 11

US-09-363-189B-6
Sequence 6, Application US/09363189B
Patent No. 624228
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, MASARAZU
APPLICANT: TONOUCHI, NAOTO
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: YOKOZUKI, KENZO
TITLE OF INVENTION: XYLTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
FILE REFERENCE: 0010-1024-0
CURRENT APPLICATION NUMBER: US/09/363, 189B
CURRENT FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: JP10-216047
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent version 3.0
SEQ ID NO 6
LENGTH: 262
TYPE: PRT
ORGANISM: Gluconobacter oxydans
US-09-363-189B-6

Query Match 22.4%; Score 292.5; DB 4; Length 262;
Best Local Similarity 31.6%; Pred. No. 2.5e-24;
Matches 86; Conservative 41; Mismatches 110; Indels 35; Gaps 7;

6 RSVAGLVAVITGASGGLTAERLVGOGASAVLLDLPNSG---GEOAKKLGNNCEAPAD 62
3 KKEGKQKLVCTAGAGNIGLTAIRLAEFGTAIALLMMNRALKEARSAVEKGEARSTYV 62
63 ADVTSEKDVOTATLALAKGFRGVAVNCAGIYAVASKTYNLKKGOTHTLEDFORVLDVNL 122
63 CDVTSEAVITGVDVSRDKIDLEFNAGYOGA-----FAYVDYPSDDFARVLTINV 117
123 MGFENVIRLVAGEM-GONEPDGQGVYIINTASVAFEGOVQAAVSASKGIVGMLPI 181
118 TGAFFHVLKAVSRQMTITN-----YGRIVNTASMGVKGPPMMAAYASGSKAIIALTET 170
182 IARLAPIGIRVMTIAPGL-----GTLTSLPEKVCNFIASQVPP 225
171 AALDLAYNINIKVNAISPGYMGPGFMERQVELAKQVSGYFTIDPKVYAAQOMIGSVPM-R 229
226 RLGGDPAEYAHVQAII--ENPFLNGEVIRLDG 255

Db 230 RYGDINEIPGVAVAFLLGDSSFMGTGVALPIAG 261

RESULT 12
5229279-7
Patent No. 5229279
APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
TITLE OF INVENTION: METHOD FOR PRODUCING NOVEL POLYESTER
BIOPOLYMERS
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/556,535
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 67,695
FILING DATE: 29-AUG-1987
SEQ ID NO: 7
LENGTH: 246
5229279-7

Query Match 22.0%; Score 287.5; DB 6; Length 246;
Best Local Similarity 31.9%; Pred. No. 8.1e-24;
Matches 81; Conservative 45; Mismatches 109; Indels 19; Gaps 7;

12 VAVITGASGGLTAERLVGOGASAVLLDLPNSGGE---AQAKKIGNNCEVFPADYTS 67
5 IAYVGGMGIGITAIQKRLANGFRVYVAGCGPNSPREKMLEQKALGFDFIASEGVAD 64
68 EKDVTALALAKGFRGVAVNCAGIYAVASKTYNLKKGOTHTLEDFORVLDVNMGTENV 127
65 WDKTKIARDKYKSEFGEVDVLIINAGI---TRDVFERK---MTADMDAVIDTSLTLEN 118
128 VIRLVAGEMQNEPDGQGVYIINTASVAFEGOVQAAVSASKGIVGMLPIARDLAP 187
119 VTQVYIDMA---DRGV--GRIVNISVNGQKQFOGTNTSTAKAGLHGFTMALAEVA 172
188 PIGIVMTIAPGLFGTPLTSLPEKVCNFIASQVPPSRLGDPAEYAHVQAII--ENPF 245
173 TKGVAVNVSPGYIATIDVKAIRQDVLDKIVAITPV-KRGLPQELNISICAMLSSESGF 231
246 LNGEVIRLDGATR 259
232 STGADFSINGLHM 245

RESULT 13
US-08-375-962B-13
Sequence 13, Application US/08375962B
Patent No. 5731195
GENERAL INFORMATION:
APPLICANT: SIMON, ANDRAS; HELLMAN, ULF; WERNSTEDT,
APPLICANT: CHRISTER, ERIKSSON, ULF.
TITLE OF INVENTION: Isolated Nucleic Acid Molecule
TITLE OF INVENTION: Which Codes for A 32 kDa Protein Having 11-CIS Retinol
TITLE OF INVENTION: Delayedrogenase Activity and Which Associates With P63,
TITLE OF INVENTION: a Portion of a Retinol Binding Protein Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect (ASCII standard)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,962B
FILING DATE: 20-January-1995
CLASSIFICATION: 435

Thu Jun 26 06:55:07 2003

us-09-931-186-4.ra1

Page 5

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,035
FILING DATE: 28-JUL-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9414622.2
FILING DATE: 20-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB95/01678
FILING DATE: 17-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT.132
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713.787.1400
TELEFAX: 713.787.1440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-793-035-9
```

```
Query Match      22.7%; Score 296; DB 3; Length 315;
Best Local Similarity 30.9%; Pred. No. 1.4e-24;
Matches 81; Conservative 44; Mismatches 115; Indels 22; Gaps 6;

QY 4 AVRSVGLVAVITGSGSLGATAEVLVGGASAVLLDPRNGGGA-----QAKLGNNC 58
DB 66 AVPKVESPVVVVVGASRGIGKAIALSL-GKAGCKVLVNVARSAREBEVSKQIEAYGQA 124
QY 59 VFAPADVTSEKDVQATLALAKGKGRVDVAVNCAGIYASVSKTYNLKGGTHLEDFORVL 118
DB 125 ITFGDVSKKADVEAMKMTAIDAMGTIDVVVNNAGITRDILLIRKKSQ-----WDEV 178
QY 119 DVNLMTENVIRLVAGEGQNEPDGQGRGVIINTSYAAAEFGQVGAAYASAKSGIYGM 178
DB 179 DNLGVFLCTQATKIRMKK-----RKRGIINIASVGLIGNIGQANYAAAKAGVIGF 232
QY 179 TLPIADLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFSLGDPAEYAHVQ 238
DB 233 SKTAAREGASRNINNVVCPGFIAISDMTAKIGEDMEKTLIGTIPL-GRYGQPEDVAGIVE 291
QY 239 AITENP---FLNGEVIRLDGAI 257
DB 292 FLALSPAASYITGQAFITDGGI 313
```

```
RESULT 9
US-08-793-035-10:
Sequence 10, Application US/08793035
Patent No. 6011201
GENERAL INFORMATION:
APPLICANT: Slabas, Antoni R.
APPLICANT: White, Andrew
APPLICANT: Chase, Dianne
APPLICANT: Elborough, Kelvin
APPLICANT: Fentem, Phillip A.
TITLE OF INVENTION: B-ketocacyl ACP Reductase Genes From
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,035
FILING DATE: 28-JUL-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9414622.2
FILING DATE: 20-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB95/01678
FILING DATE: 17-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT.132
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713.787.1400
TELEFAX: 713.787.1440
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-793-035-10
```

```
Query Match      22.7%; Score 296; DB 3; Length 315;
Best Local Similarity 30.9%; Pred. No. 1.4e-24;
Matches 81; Conservative 44; Mismatches 115; Indels 22; Gaps 6;

QY 4 AVRSVGLVAVITGSGSLGATAEVLVGGASAVLLDPRNGGGA-----QAKLGNNC 58
DB 66 AVPKVESPVVVVVGASRGIGKAIALSL-GKAGCKVLVNVARSAREBEVSKQIEAYGQA 124
QY 59 VFAPADVTSEKDVQATLALAKGKGRVDVAVNCAGIYASVSKTYNLKGGTHLEDFORVL 118
DB 125 ITFGDVSKKADVEAMKMTAIDAMGTIDVVVNNAGITRDILLIRKKSQ-----WDEV 178
QY 119 DVNLMTENVIRLVAGEGQNEPDGQGRGVIINTSYAAAEFGQVGAAYASAKSGIYGM 178
DB 179 DNLGVFLCTQATKIRMKK-----RKRGIINIASVGLIGNIGQANYAAAKAGVIGF 232
QY 179 TLPIADLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFSLGDPAEYAHVQ 238
DB 233 SKTAAREGASRNINNVVCPGFIAISDMTAKIGEDMEKTLIGTIPL-GRYGQPEDVAGIVE 291
QY 239 AITENP---FLNGEVIRLDGAI 257
DB 292 FLALSPAASYITGQAFITDGGI 313
```

```
RESULT 10
US-09-134-001C-4512
Sequence 4512, Application US/09134001C
Patent No. 6360370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4512
LENGTH: 263
```

Thu Jun 26 06:55:07 2003

us-09-931-186-4.ral

Page 4

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,225
FILING DATE: 12-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/55209
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-815-225-4

Query Match 23.0%; Score 300; DB 4; Length 255;
Best Local Similarity 33.2%; Pred. No. 3,5e-25;
Matches 85; Conservative 48; Mismatches 103; Indels 20; Gaps 8;

QY 5 VASVGLVAVITGASGIGLATAERLVGQASAVLLDLPNSGSGAOKKLNCCVFAPAD 64
DB 1 MNDLSKVTIITGARGIGLAEARQAVAAARVADVLDDEGATATLGGAPAYCHLD 60
QY 65 VSEKDVOTLALAKGKGRVDVAVNCAGIAVASTYMLKKQCTITLDDFORVLDVNLG 124
DB 61 VIEEDMORVAVYAAEEFSGVDGLVNNAGISTGMFL-----ETSEVERFRVVDINLTG 114
QY 125 TENVIRLVAGMGONEPDGQGVYINTASVAAFEGGVQAAVSASKGIYGMTLPAR 184
DB 115 VILGKMTVIRPAW-----KQAG--GSLVNSSAAGMLGLTSSYASKMGVGLSKLAAY 168
QY 185 DLAPIGIRVMTIAPGLFGTPLL--TSLPEKVCNFIASQVPPFSRIG-DPAFAHLYQAL 241
DB 169 ELGTDRIKRVNSVHPGKTYTPMTAETGIRGEGNY--PMTPM-GRVGNBEGELAGAVVKLL 225
QY 242 E--NPLNGEIVRLDG 255
DB 226 SDTSSVTGALAVDG 241

RESULT 7
US-08-440-856A-4
Sequence 4, Application US/08440856A
Patent No. 5750873
GENERAL INFORMATION:
APPLICANT: DELLAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA

ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-440-856A-4

Query Match 23.0%; Score 299.5; DB 1; Length 333;
Best Local Similarity 32.5%; Pred. No. 6,1e-25;
Matches 92; Conservative 46; Mismatches 106; Indels 39; Gaps 5;

QY 6 RSVKGLVAVITGASGIGLATAERLVGQASAVLLDLPNSGSGAOKKLNCCVFAPAY 65
DB 50 KRLGKVAIVTGGARGIGLAEIVRLFKHGAKVVIADIDAAAGLAAAGPHGVEYRCV 109
QY 66 TSEKDVOTLALAKGKGRVDVAVNCAGIAVASTYMLKKQCTITLDDFORVLDVNLG 125
DB 110 SVEEDVRAVRAVYARIGRDVLCNNAGV-LGROTAAKILISFDGSEFDRVLRVALGA 168
QY 126 FNVIRLVAGMGONEPDGQGVYINTASVAAFEGGVQAAVSASKGIYGMTLPAD 185
DB 169 ALGKHAALMTOR-----FAGSIISVASVAGVLGIPHAATASKHAIVGLTKNAEE 222
QY 186 LAPGIRVMTIAPGLFGTPLL-----TSLP-----EKYC 214
DB 223 LGAGIRVNCISPPGAVTPIILNMRGSHASTADADADIDDIAPSPQVEKNEBYV 282
QY 215 NFIAQVPPFSRIGDPAEYAHLYQALLENPLNGEIVRLDGAI 257
DB 283 RGLATLKGATLRPRDIAE-AALFLASDSRYISGHNLYVDGVG 324

RESULT 8
US-08-793-035-9
Sequence 9, Application US/08793035
Patent No. 6011201
GENERAL INFORMATION:
APPLICANT: Slabas, Antoni R.
APPLICANT: White, Andrew
APPLICANT: Chase, Dianne
APPLICANT: Elborough, Keiran
APPLICANT: Fentem, Phillip A.
TITLE OF INVENTION: B-Retocacyl ACP Reductase Genes From
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

Thu Jun 26. 06:55:07 2003

us-09-931-186-4.rai

Page 3

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347, 878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
US-09-347-878-50

Query Match 99.68; Score 1299; DB 4; Length 261;
Best Local Similarity 99.68; Pred. No. 4,3e-136;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAVRSYGLVAVITGSGASGLGATAEFLVGGASAVLLDLPNSGGEAQAQKLGNNCF 60
DB 1 MAAACRSYGLVAVITGSGASGLGATAEFLVGGASAVLLDLPNSGGEAQAQKLGNNCF 60
QY 61 APADYTSKEDVOTATLAKGKRGYDVAVNCAGIAVASKTYNKKGOTHTLEDFQRLDV 120
DB 61 APADYTSKEDVOTATLAKGKRGYDVAVNCAGIAVASKTYNKKGOTHTLEDFQRLDV 120
QY 121 NLMGFENYIRLVAGEMGONEPDGQGRVITNTASVAEFEGVQAAYASAKSGIVGNTL 180
DB 121 NLMGFENYIRLVAGEMGONEPDGQGRVITNTASVAEFEGVQAAYASAKSGIVGNTL 180
QY 181 PIARDLADIGIRVMTIADLFGTPLTSLPEKVCNFTLASOVPPSPSLGDPPEYAHVQAI 240
DB 181 PIARDLADIGIRVMTIADLFGTPLTSLPEKVCNFTLASOVPPSPSLGDPPEYAHVQAI 240
QY 241 IENPFLNGEVRILDGAIKMP 261
DB 241 IENPFLNGEVRILDGAIKMP 261

RESULT 4

US-08-980-832-41
Sequence 41, Application US/089808328
Patent No. 6291204
GENERAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Tsysanukov, Yuri
TITLE OF INVENTION: Improved Fermentative Carotenoid Production
FILE REFERENCE: Improved Fermentative Carotenoid
CURRENT APPLICATION NUMBER: US/08/980, 832B
CURRENT FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41
LENGTH: 388
TYPE: PRT
ORGANISM: Flavobacterium sp. R1534
US-08-980-832-41

Query Match 51.0%; Score 664.5; DB 4; Length 388;
Best Local Similarity 55.5%; Pred. No. 2,3e-65;
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VGLVAVITGSGASGLGATAEFLVGGASAVLLDLPNSGGEAQAQKLGNNCFAPADYTS 67
DB 143 IGRVYVVTGASGLGASGLGATAEFLVGGASAVLLDLPNSGGEAQAQKLGNNCF 196
QY 68 EKDVOATLALAKGKRGYDVAVNCAGIAVASKTYNKKGOTHTLEDFQRLDVNLGTFN 127
DB 197 ARAAQTAIALADRFRLDGLVNCAGIAFAERM--LGRGPRGLDSFAFAVAINIGSFN 254
QY 128 VIRLVAGEMGONEPDGQGRVITNTASVAEFEGVQAAYASAKSGIVGNTLPIARDIA 187
DB 255 MARLAAEMARNEPRV-GERGVITVNTASIAADGQIGVQAAYASAKSGIVGNTLPIARDIA 313
QY 188 PIGIRVMTIADLFGTPLTSLPEKVCNFTLASOVPPSPSLGDPPEYAHVQAIENPFLN 247

DB 314 RHGIRVMTIADLFGTPLTSLPEKVCNFTLASOVPPSPSLGDPPEYAHVQAIENPFLN 373
QY 248 GEYIRLDGAIKMP 261
DB 374 GEYIRLDGAIKMP 387

RESULT 5

US-09-239-052-2
Sequence 2, Application US/09239052
Patent No. 6346395
GENERAL INFORMATION:
APPLICANT: Holmes, David J.
APPLICANT: Zhong, Yiyi
APPLICANT: Debouck, Christine
APPLICANT: Jaworski, Deborah D.
APPLICANT: Wang, Min
APPLICANT: Warren, Richard L.
APPLICANT: Kosmatka, Anna L.
APPLICANT: McDevitt, Damien
APPLICANT: Ingraham, Karen A.
APPLICANT: Chalke, Alison F.
APPLICANT: So, Chi Young
APPLICANT: Wallis, Nicola G.
APPLICANT: Pearson, Stewart C.
TITLE OF INVENTION: FabG
FILE REFERENCE: GM10191
CURRENT APPLICATION NUMBER: US/09/239, 052
CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 243
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-239-052-2

Query Match 25.0%; Score 326.5; DB 4; Length 243;
Best Local Similarity 35.1%; Pred. No. 3,7e-28;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

QY 15 ITGASGLGATAEFLVGGASAVLLDLPNSGGE-----AQAKKLGNNCFAPADYTS 68
DB 10 ITGSSRSIGLAIHAKFQAQANIVL-----NSRGLISELLAEFSNGIKVPSISGVSDR 65
QY 69 KDVOATLALAKGKRGYDVAVNCAGIAVASKTYNKKGOTHTLEDFQRLDVNLGTFN 128
DB 66 ADARMDIDQAIELGSDVAVNNAGI--TDDTLMLKV---TEADEKVKVNLGAFNM 119
QY 129 IRLVAGEMGONEPDGQGRVITNTASVAEFEGVQAAYASAKSGIVGNTLPIARDIA 188
DB 120 TQSVL-----KPMKARREGATIMSSVGLMGVIGQANTAAKAGLIGFTKSVAREVAS 173
QY 189 IGRVMTIADLFGTPLTSLPEKVCNFTLASOVPPSPSLGDPPEYAHVQAIENPFLN 248
DB 174 RNIRVNTIAPQMISDMLTSLDKIKRATLAQIPM-KEFGQAEQVADLFTVLAGODYLTG 232
QY 249 EYIRLDGAIKMP 259
DB 233 QVIAIDGGLSM 243

RESULT 6

US-08-815-225-4
Sequence 4, Application US/08815225
Patent No. 6268479
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Yan, Shi Du
TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE
TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING
TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

ALIGNMENTS

RESULT 1

US-08-815-225-2

; Sequence 2, Application US/08815225

; Patent No. 6268479

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; APPLICANT: Yan, Shi Du

; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/815,225

; FILING DATE: 12-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/55209

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 391-0525

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ. ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 261 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-815-225-2

Query Match 99.6%; Score 1299; DB 4; Length 261;
Best Local Similarity 99.6%; Pred. No. 4.3e-136;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAAVSYKGLVAVITGASGLGLATAERLVGGASAVLLDLPNSGGEAQAARKLGNVCVF 60
DB 1 MAAACRSYKGLVAVITGASGLGLATAERLVGGASAVLLDLPNSGGEAQAARKLGNVCVF 60
QY 61 APADVTSEKDVOTALALAKGKFGVDVAVNAGIAVASKTYNKKGTHTLEDFORVLDV 120
DB 61 APADVTSEKDVOTALALAKGKFGVDVAVNAGIAVASKTYNKKGTHTLEDFORVLDV 120
QY 121 NLMGTFNIVRLVAGMGONEDPDGQGRVITINTASVAAFEGVGOAAVSASKGGIVGML 180
DB 121 NLMGTFNIVRLVAGMGONEDPDGQGRVITINTASVAAFEGVGOAAVSASKGGIVGML 180
QY 181 PIARDLAPIGIRVMTIAPGLTGLTSLPERKVCNFLASQVPPSRSLGDPAEVAHLVQAI 240
DB 181 PIARDLAPIGIRVMTIAPGLTGLTSLPERKVCNFLASQVPPSRSLGDPAEVAHLVQAI 240
QY 241 IENPFLNGEVIRLDGAIKMP 261
DB 241 IENPFLNGEVIRLDGAIKMP 261

US-08-815-225-3

; Sequence 3, Application US/08815225

; Patent No. 6268479

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; APPLICANT: Yan, Shi Du

; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/815,225

; FILING DATE: 12-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/55209

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 391-0525

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ. ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 261 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-815-225-3

Query Match 99.6%; Score 1299; DB 4; Length 261;
Best Local Similarity 99.6%; Pred. No. 4.3e-136;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAAVSYKGLVAVITGASGLGLATAERLVGGASAVLLDLPNSGGEAQAARKLGNVCVF 60
DB 1 MAAACRSYKGLVAVITGASGLGLATAERLVGGASAVLLDLPNSGGEAQAARKLGNVCVF 60
QY 61 APADVTSEKDVOTALALAKGKFGVDVAVNAGIAVASKTYNKKGTHTLEDFORVLDV 120
DB 61 APADVTSEKDVOTALALAKGKFGVDVAVNAGIAVASKTYNKKGTHTLEDFORVLDV 120
QY 121 NLMGTFNIVRLVAGMGONEDPDGQGRVITINTASVAAFEGVGOAAVSASKGGIVGML 180
DB 121 NLMGTFNIVRLVAGMGONEDPDGQGRVITINTASVAAFEGVGOAAVSASKGGIVGML 180
QY 181 PIARDLAPIGIRVMTIAPGLTGLTSLPERKVCNFLASQVPPSRSLGDPAEVAHLVQAI 240
DB 181 PIARDLAPIGIRVMTIAPGLTGLTSLPERKVCNFLASQVPPSRSLGDPAEVAHLVQAI 240
QY 241 IENPFLNGEVIRLDGAIKMP 261
DB 241 IENPFLNGEVIRLDGAIKMP 261

RESULT 3
US-09-347-878-50
; Sequence 50, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:


```

FT      /note="alpha helix region A"
FT      Region
FT      190..196
FT      /note="beta sheet region F"
FT      Region
FT      204..218
FT      /note="alpha helix region F"
FT      247..252
FT      /note="beta sheet region G"
XX      MO9954347-A2.
XX      28-OCT-1999.
XX      19-APR-1999; 99MO-EP02610.
XX      17-APR-1998; 98US-0082257.
XX      (HORM-) INST HORMON & FORTPFLANZUNGSFORSCHUNG GM.
XX      PI Iwells R, Spiess A, Balvers M, Jaehner D, Hansis C;
XX      WPI; 2000-052699/04.
XX      DR N-PSDB; AA234663.
XX      Novel differential display reverse transcription PCR method used to
XX      detect genes expressed in mutant tissues
XX      Claim 4; Fig 2; 40pp; English.
XX      This sequence represents murine Alzheimer-associated beta-amyloid
XX      binding protein (ERAB, see AA332339), a novel member of the SCAD
XX      (short chain alcohol dehydrogenase) family of steroid metabolizing
XX      and related enzymes. The sequence was deduced from cDNA (see
XX      AA344663) identified using a novel differential display RT-PCR method
XX      for analysis of w/w mouse testis gene products. ERAB is
XX      specifically upregulated in the testicular Leydig cells of w/w
XX      azoospermic mutant mice, suggesting an important role in the
XX      establishment and support of spermatogenesis. The invention also
XX      relates to vectors, host cells, methods for expressing the ERAB
XX      nucleic acid, and antibodies. The nucleic acid and protein are
XX      useful e.g. as markers for testicular development.
XX      Sequence 260 AA:
XX      Query Match 88.38; Score 1152; DB 21; Length 260;
XX      Best Local Similarity 88.08; Pred. No. 6.6e-105;
XX      Matches 227; Conservative 18; Mismatches 13; Indels 0; Gaps 0;
QY      4 ACRSVKGIIVAVITGASGLATATERTLVGGASAVLADLPSNGSGEAOAKKLGNNCFAPA 63
DB      3 AVRSVKGIIVAVITGASGLATATERTLVGGASAVLADLPSNGSGEAOAKKLGSCIFAPA 62
QY      64 DVTSEKDVOTALALAKRGFRVDVAVNCAGIIVASAKTYNKKGGTHTLEDFOFVLDVNL 123
DB      63 NVTSEKDVOTALALAKRGFRVDVAVNCAGIIVASAKTYNKKGGTHTLEDFOFVLDVNL 122
QY      124 GTFNVIRLVAGEMQNEPDGSGGVIINTASVAFGGVGOQAYASAKGIVGMTPIA 183
DB      123 GTFNVIRLVAGEMQNEPDGSGGVIINTASVAFGGVGOQAYASAKGIVGMTPIA 182
QY      184 RDLAPGIGIRVMTIAPGLTSLPEKVNFLASGVPPSRSLGDAEYVAHLVQATIEEN 243
DB      183 RDLAPGIGIRVMTIAPGLTSLPEKVNFLASGVPPSRSLGDAEYVAHLVQATIEEN 242
QY      244 PFLNGEVRRLDGAIRMP 261
DB      243 PFLNGEVRRLDGAIRMP 260

```

```

XX      25-MAR-1999 (first entry)
XX      Fragment of human secreted protein encoded by gene 8.
XX      Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX      diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX      developmental abnormality; foetal deficiency; blood; allergy; renal;
XX      immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX      inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
XX      cognitive disorder; schizophrenia; prostate; obesity; osteoarthritis;
XX      osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX      endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX      Homo sapiens.
XX      WO9842738-A1.
XX      01-OCT-1998.
XX      19-MAR-1998; 98MO-US05311.
XX      30-MAY-1997; 97US-0050937.
XX      21-MAR-1997; 97US-0041276.
XX      21-MAR-1997; 97US-0041277.
XX      21-MAR-1997; 97US-0041281.
XX      21-MAR-1997; 97US-0042344.
XX      30-MAY-1997; 97US-0048069.
XX      30-MAY-1997; 97US-0048094.
XX      30-MAY-1997; 97US-0048095.
XX      30-MAY-1997; 97US-0048096.
XX      30-MAY-1997; 97US-0048099.
XX      30-MAY-1997; 97US-0048131.
XX      30-MAY-1997; 97US-0048135.
XX      30-MAY-1997; 97US-0048154.
XX      30-MAY-1997; 97US-0048160.
XX      30-MAY-1997; 97US-0048186.
XX      30-MAY-1997; 97US-0048187.
XX      30-MAY-1997; 97US-0048188.
XX      30-MAY-1997; 97US-0048350.
XX      30-MAY-1997; 97US-0048351.
XX      30-MAY-1997; 97US-0048352.
XX      30-MAY-1997; 97US-0048355.
XX      05-AUG-1997; 97US-0054804.
XX      (HUMA-) HUMAN GENOME SCI INC.
XX      Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA;
XX      Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;
XX      Rosen CA, Ruben SM, Shi Y, Young P;
XX      WPI; 1999-070066/06.
XX      N-PSDB; AA00618.
XX      New isolated human genes and the secreted polypeptides they encode -
XX      useful for diagnosis and treatment of e.g. cancers, neurological
XX      disorders, immune diseases, inflammation or blood disorders
XX      Disclosure; Page 11; 385pp; English.
XX      This sequence represents a fragment of a secreted human protein encoded
XX      by the nucleic acid molecule detailed in the descriptor line. The gene
XX      can be used to generate fusion proteins by linking to the gene to a
XX      human immunoglobulin Fc portion (e.g. AA00602) for increasing the
XX      stability of the fused protein as compared to the human protein only.
XX      The invention relates to 87 novel genes and their fragments (nucleic
XX      acid sequences: AA00611-X00724; amino acid sequences AA067807-W68004)
XX      which are useful for preventing, treating or ameliorating medical
XX      conditions e.g. by protein or gene therapy. Also, pathological
XX      conditions can be diagnosed by determining the amount of the new
XX      polypeptides in a sample or by determining the presence of mutations in
XX      the new polynucleotides. Specific uses are described for each of the 87
XX      polynucleotides, based on which tissues they are most highly expressed in

```

```

RESULT 3
AA067934
ID      AA067934 standard; 227 AA.
XX      AC      AA067934;

```

CC (see AAX00611 for described uses).

XX Sequence 227 AA:

Query Match 86.9%; Score 1134; DB 20; Length 227;

Best Local Similarity 99.6%; Pred. No. 3.2e-103;

Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 35 ASAYLIDLPSNGSGDAQAKKLGNNCVAPADVTSEKVVQRLALAKKFGKRVAVVACAI 94
 DB 1 ASAYLIDLPSNGSGDAQAKKLGNNCVAPADVTSEKVVQRLALAKKFGKRVAVVACAI 60
 QY 95 AVAKTNTLKKGGHTLEDFORVLDVNLMTGFNVIRLVAGEMGNPDGSGRGVLIINTA 154
 DB 61 AVAKTNTLKKGGHTLEDFORVLDVNLMTGFNVIRLVAGEMGNPDGSGRGVLIINTA 120
 QY 155 SVAAFEGQVGAAYASAKSGIVGNTLPIDAPLIGIRVKTAPGLFPTPLTSLPEKYR 214
 DB 121 SVAAFEGQVGAAYASAKSGIVGNTLPIDAPLIGIRVKTAPGLFPTPLTSLPEKYR 180
 QY 215 NFLLSOVPEPSRLGDPAPAYAHVQATLENPFINGEVRIDGAIKMP 261
 DB 181 NFLLSOVPEPSRLGDPAPAYAHVQATLENPFINGEVRIDGAIKMP 227

RESULT 4

ABB62988 ID ABB62988 standard; Protein: 255 AA.

AC ABB62988;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 15756.

KW Drosophila: developmental biology; cell signalling; insecticide; pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PMD, Myers EW;

PI WPI; 2001-656660/75.

DR N-PSDB; ABL07091.

PT New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signalling and cell-cell

PT interactions -

PS Disclosure; SEQ ID NO 15756; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABLU6176-ABU30511), expressed DNA

CC sequences (ABU1840-ABU16175) and the encoded proteins

CC (ABU57737-ABU72072).

CC The sequence data for this patent did not form part of the printed

CC specification, and was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 255 AA:

Query Match 70.2%; Score 916; DB 22; Length 255;

Best Local Similarity 69.3%; Pred. No. 1e-61; Indels 0; Gaps 0;

Matches 176; Conservative 29; Mismatches 49; Indels 0; Gaps 0;

QY 8 VGLVAVITGGASGIGLTAERLVGOGASAVLLDLPNSGGEQAQKLGNNCVAPADVT 67
 DB 2 IKNVSLVTGGASGIGLTAERLVGOGASAVLLDLPNSGGEQAQKLGNNCVAPADVT 61
 QY 68 EKDVOTLALAKKRGKRVAVVACAIKGVASKTNTLKKGGHTLEDFORVLDVNLMTGF 127
 DB 62 EKDVSAALQTAQKRGKRVAVVACAIKGVASKTNTLKKGGHTLEDFORVLDVNLMTGF 121
 QY 128 VIRLVAGEMGNPDGSGRGVLIINTASVAAFEQVGAAYASAKSGIVGNTLPIDAPL 187
 DB 122 VIRLVAGEMGNPDGSGRGVLIINTASVAAFEQVGAAYASAKSGIVGNTLPIDAPL 181
 QY 188 PIGIRVMTAPGLFPTPLTSLPEKYRNFLLSOVPEPSRLGDPAPAYAHVQATLEN 247
 DB 182 TOGIRICTIAPGLFPTPLTSLPEKYRNFLLSOVPEPSRLGDPAPAYAHVQATLEN 241
 QY 248 GEVIRIDGAIKMP 261
 DB 242 GEVIRIDGAIKMP 255

RESULT 5

AAM06513 ID AAM06513 standard; Protein: 388 AA.

AC AAM06513;

DT 08-MAR-1997 (first entry)

DE Flavobacterium ORF-5 gene product.

KW Carotenoid; lycopen; beta-carotene; echinenone; canthaxanthin;

KW zeaxanthin; adonixanthin; astaxanthin.

OS Flavobacterium sp. R1534 WT (ATCC 21586).

PN EP747483-A2.

PD 11-DEC-1996.

PF 29-MAY-1996; 96EP-0108556.

PR 09-JUN-1995; 95EP-0108888.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Hohmann H, Pasamontes L, Tessier M, Van Loon A;

PI WPI; 1997-023160/03.

DR N-PSDB; AAT45143.

PT Flavobacterium gene sequences encoding carotenoid biosynthesis

PT enzymes - for the production of carotenoid(s), useful in foods and

PT animal feeds

PS Example 2; Fig 7; 80pp; English.

CC A polypeptide (AAM06513) showing approx. 30% homology to

CC streptomycete polyketide synthases was identified as the product

CC of ORF-5 from a carotenoid gene cluster (see also AAT45143) of

CC Flavobacterium sp. R1534. 5 Other open reading frames of the

CC gene cluster coded for carotenoid biosynthetic enzymes (see also

CC AAM06515-18 and AAM06871) and can be used to produce carotenoids in

CC transformed host cells.

CC Sequence 388 AA;

	Query Match	51.2%	Score 668.5	DB 18	Length 388;
	Best Local Similarity	55.5%*	Pred No. 3.7e-57;		
	Matches 141;	Conservative 36;	Mismatches 68;	Indels 9;	Gaps 3
QY	8 VKGLVAVITGGASGIGLTAERLVVGOGASAYLLDLPNSGGEQAOKKIGNNCVPADYTS	67			
	::::: :::				
Db	143 IEGRFVVYVGAAGSAGASARMLAOGGAKVYLALD----	AEEKDAPEGAVHAACDVTD	196		
	::: :::				
QY	68 EKVQFATALAKGFEPGRVDVAVNCAGIVASKTYNLKKGTHTLEDFOFLVDNLNGTGN	127			
	::: :::				
Db	197 ATAAQPAIALMDTRFGRLDGLVNCAGIAPAEEM--LGDRGHGISDFARA VTI NLGSFN	254			
	::: :::				
QY	128 VTLVAGEGQNRPDDGGRGVIINTLSAVAPEEQGVGAASAASKGIYMTPIARDLA	187			
	::: :::				
Db	255 MAQLAAEAMRNSEPVN-GERGYVTNTASTAADGGIGVATASKAAGVACGMTIPMARDLA	313			
	::: :::				
QY	188 PIGIRVMTIAPGLEFTPLITSPEKYRNFILASQVFPPSRLCDPAAEVIAHQVAINENFVN	247			
	::: :::				
Db	314 RHGIRVMTIAPGIFRTPLEGSLPOVDOSLAGAAVFPESRLGPESPETVALLIHIIITPMNLN	373			
	::: :::				
QY	248 GEVIRLDGARIMQP	261			
	::: :::				
Db	374 GEVIRLDGALLMAP	387			

RESULT 6
ABP28011
ID ABP28011 standard; Protein: 244 AA.

AC ABP28011;

DT 02-JUL-2002 (first entry)

XX New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -

PS Claim 1; Page 3542; 4525bp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus pyogenes (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and anti-inflammatory
CC activity. (1), nucleic acids encoding (1), ABN65044-ABN71526 and
CC antibodies that bind (1) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (1) are used to detect Streptococcus in a
CC biological sample. (1) is used to determine whether a compound binds to
CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (1) may be used to recombinantly produce (1) and may be
CC used in gene therapy. Antibodies to (1) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.

XX Sequence 243 AA;

Query Match 27.2%; Score 355; DB 23; Length 243;
Best Local Similarity 35.4%; Pred. No. 1.2e-26;
Matches 92; Conservative 43; Mismatches 99; Indels 26; Gaps 6;

QY 8 VGVIAVITGGASGGLTAERLVGGASAVLLDLPNSGGEAOKRL-----GNNCFE 60
DB 3 IKGNI-FTTGSTRGIGLMAHGFASLENIYL-----NGRAISEBELVASTDYGIVVT 56
QY 61 APADYTSERDYOTALAKKRGFRVAVNCAGIAVASKTYNLKGGTHLEDFORVLDV 120
DB 57 ISGDVSEASEAKRMVNEAIESISIDVLYNNAGIT-----NDKMLKMTEDDERVYKI 110
QY 121 NLMGFNRYLVAGMGONEPDGGRGVIINTASVAAFEGOVGAASASKGIVGWT 180
DB 111 NLTGAVNMTQSVL-----KPKITAKQGAIIIVSSVGLTGNIGQANTAAASKAGMIGTK 164
QY 181 PIARDIAPIGIRVMTIAPGLFETPLITSPEKVRNFASQVPEPSRLDPAEVAHLVQAI 240
DB 165 SVAREVAARNICVNMIAFGFIESDMTGVLPKMGQILSQIPM-KRICKAQEVAHLASFL 223
QY 241 TENPFGNEVIRLDGAIRMQ 260
DB 224 VEODYITGGVIAIDGGMTMQ 243

RESULT 8

ID AAM80670 standard; Protein; 243 AA.

XX AAM80670;

XX 24-DEC-1998 (first entry)

XX S. pneumoniae fatty acid biosynthesis protein.

XX Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip;

XX virulence; antibody; infection; detection; treatment; hypothetical;

XX cell wall biosynthetic, external target; minimal gene set protein.

XX Streptococcus pneumoniae.

XX WO9826072-A1.

XX 18-JUN-1998.

XX 09-DEC-1997; 97WO-0522578.

XX 13-DEC-1996; 96US-0036281.
PR (ELI) LILLY & CO ELI.

XX Balz RH, Burgett SG, Dehoff BS, Hoskins JA, Jaskunas SR;
PI Mills SD, Norris FH, Peery RB, Rockey PK, Rostek PR;
PI Skatrud PL, Smith WC, Solenberg PJ, Treadway PJ;
PI Young Bellido ML;
DR WPI; 1998-148529/30.

XX Streptococcus pneumoniae nucleic acid sequences - used in DNA chips
PT for evaluating gene expression, and identification of virulence
PI genes

XX Claim 3; Page 270; 333p; English.

XX This sequence represents a S. pneumoniae fatty acid biosynthesis
CC protein. The invention provides DNA sequences (AAV65201 to AAV65304)
CC from the streptococcus pneumoniae genome and corresponding protein
CC sequences (AAM80605 to AAM80728). The protein sequences are classified as
CC hypothetical, cell wall biosynthetic, external target, or minimal gene
CC set proteins. A recombinant host containing a vector comprising any of
CC the above nucleic acids can be used for the recombinant expression of the
CC proteins. The invention also provides a DNA chip having arrayed on it at
CC least 15 base pair fragment of any one or more of these DNA sequences.
CC The DNA chip can be used methods for evaluating gene expression in S.
CC pneumoniae and for identifying virulence genes in S. pneumoniae.
CC Antibodies that selectively bind to the above proteins or peptide
CC fragments can be used to treat S. pneumoniae infection. The antibodies
CC can also be used to detect S. pneumoniae cells.

XX Sequence 243 AA;

Query Match 25.4%; Score 331.5; DB 19; Length 243;
Best Local Similarity 35.1%; Pred. No. 2.5e-24;
Matches 88; Conservative 37; Mismatches 103; Indels 23; Gaps 6;

QY 15 ITGASGLGATARTERLVGGASAVLLDLPNSGGE-----AQAKKIGNCCVAPADYSE 68
DB 10 ITGSSRIGIGAIATKFAKQAGANITVL-----NSRAISEBELAERSNNGIVVPSGDVDF 65
QY 69 KDVOITALAKKRGFRVAVNCAGIAVASKTYNLKGGTHLEDFORVLDVNLMTGFNV 128
DB 66 ADARFMDQAIATGSDVAVLYNNAGT--TQDTLMKK-----TADDEKYKAVNLGAFNM 119
QY 129 IRLVAGMGONEPDGGRGVIINTASVAAFEGOVGAASASKGIVGWTLPARDLAP 188
DB 120 TQSVL-----KPMKARREGAIIIVSSVGLMGNIGQANTAAASKAGIGFTKSVAREVSE 173
QY 189 IGRVMTIAPGLFETPLITSPEKVRNFASQVPEPSRLDPAEVAHLVQAIENPFLNG 248
DB 174 RNIRVNVIAPGMIESDMTALISDKIKETATLAQIPM-KEFGQAEVADLTFTLAGQDYING 232
QY 249 EVIRLDGAIRM 259
DB 233 QVIAIDGSLM 243

RESULT 9

ID AAB15706 standard; Protein; 243 AA.

XX AAB15706;

XX 07-DEC-2000 (first entry)

XX Streptococcus pneumoniae FabG polypeptide.

XX Streptococcus pneumoniae; FabG; 3-oxoacyl-acyl carrier protein reductase;

XX antibacterial; cytostatic; anticancer; cancer; gastric ulcer; gastritis;
KW Helicobacter pylori infection; microbial infection.

XX Streptococcus pneumoniae.
OS
XX WO2000044885-A1.
XX 03-AUG-2000.
XX 19-JAN-2000; 2000WO-US01131.
XX 27-JAN-1999; 99US-0239052.
XX
XX (SMK) SMITHKLINE BEECHAM CORP.
XX Holmes DJ, Mooney J, Zhong Y, Debouck C, Jaworski DD, Wang M,
PI Warren RL, Kosmatka AL, McDevitt D, Ingraham KA, Chalkier AF,
PI So CY, Wallis NG, Pearson SC;
XX MPI: 2000-482971/42.
XX N-PSDB: AAA74684.
XX
XX FabG polypeptide, isolated from Streptococcus pneumoniae, is used to
PT treat microbial diseases, identify agonists and antagonists for
PT treating microbial infections and to detect diseases associated with
PT microbial infections -
XX
XX Claim 1: Page 3; 40pp; English.
XX
XX The present sequence is a FabG (2-oxoacyl-acyl carrier protein
CC reductase) polypeptide. A full length FabG gene was isolated from a
CC Streptococcus pneumoniae 0100993 DNA library in E. coli. FabG
CC polynucleotides and polypeptides are used for detection and treatment of
CC microbial diseases. They may also be used to identify antagonists and
CC agonists which can then be used to treat microbial diseases. Compounds
CC that interfere with the initial physical interaction between a pathogen
CC and a host have been identified. The compounds are able to prevent the
CC adhesion of bacteria to mammalian extracellular proteins in wounds,
CC prevent adhesion between mammalian extracellular proteins and bacterial
CC FabG proteins which mediate tissue damage and/or to block normal
CC progression of pathogenesis in infections mediated by implantation of
CC in-dwelling devices or other surgical techniques. The FabG
CC polypeptides, polynucleotides, antagonists and agonists are especially
CC useful in the treatment of Helicobacter pylori infection. They may be
CC used to decrease H. pylori-induced cancers and to prevent, inhibit
CC and/or cure gastric ulcers and gastritis.
XX
XX Sequence 243 AA:
SQ
Query Match 25.4%; Score 331.5; DB 21; Length 243;
Best Local Similarity 35.1%; Pred. No. 2.5e-24;
Matches 88; Conservative 37; Mismatches 103; Indels 23; Gaps 6;

AAU37767
ID AAU37767 standard: Protein; 243 AA.
XX
XX AAU37767;
XX 14-FEB-2002 (first entry)
XX
XX Streptococcus pneumoniae cellular proliferation protein #196.
XX
XX Antisense; prokaryotic cellular proliferation protein;
XX antibiotic; antibacterial; drug design.
XX
XX Streptococcus pneumoniae.
OS
XX
XX WO200170955-A2.
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US09180.
XX
XX 21-MAR-2000; 2000US-191078P.
XX 23-MAY-2000; 2000US-206848P.
XX 26-MAY-2000; 2000US-207727P.
XX 23-OCT-2000; 2000US-242578P.
XX 27-NOV-2000; 2000US-253625P.
XX 22-DEC-2000; 2000US-257931P.
XX 16-FEB-2001; 2001US-269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Traxler JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX MPI: 2001-611495/70.
XX N-PSDB: AAS55626.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
PT
XX
XX Example 3: Seq ID No 13360; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes' their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_bct_sequences.
XX
XX Sequence 243 AA:
SQ
Query Match 25.4%; Score 331.5; DB 22; Length 243;
Best Local Similarity 35.1%; Pred. No. 2.5e-24;
Matches 88; Conservative 37; Mismatches 103; Indels 23; Gaps 6;

Db AAKAKRIIQAIAELGSDVVLNNNGI--TQDTLMLKM----TEADPEKVLKVLTGAFNN 118

QY 125 IRLVAGEMGNPPDGGQRGVITINTASYAAEEGVQGAASASNGCIYGVITLPIARDLAP 168

Db 120 TQSVL-----KPMKAREGAIINNSVYGLMGNIQANPAASPAAGLIGTKSAAREVAS 173

QY 189 IGRVYTIAPGLFGTGPLLTSLPEKRNFLASQVPEPRLGDPAPAYALHVAIIENPFLG 248

Db 174 RNRIRNVAVIAPGIESDMTALLSDRIKENTLQIDPM-KEFGQAEGVADLTVEFLAGQCYLG 232

QY 249 EYIRLDGAI RM 259

Db 233 QVTAIDGGLSM 243

RESULT 11

AAU37988

ID AAU37988 standard; Protein; 243 AA.

AAU37988;

14-FEB-2002 (first entry)

Streptococcus pneumoniae cellular proliferation protein #417.

Antisense: prokaryotic cellular proliferation protein;

antibiotic; antibacterial; drug design.

Streptococcus pneumoniae.

WO200170955-A2.

27-SEP-2001.

21-MAR-2001; 2001MO-US09180.

21-MAR-2000; 2000US-191078P.

23-MAY-2000; 2000US-206848P.

26-MAY-2000; 2000US-207727P.

23-OCT-2000; 2000US-242578P.

27-NOV-2000; 2000US-253625P.

22-DEC-2000; 2000US-257931P.

16-FEB-2001; 2001US-269308P.

(ELIT-) ELITRA PHARM INC.

Haselbeck R, Ohlsen KL, Zyskind JM, Wall D, Trawick JD, Carr GJ; Yamamoto RT, Xu HR;

WPI: 2001-611495/70.

N-PSDB: AAS55847.

New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -

Example 3; Seq ID No 13581; 511pp; English.

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part

[illegible]

CC acids are useful for detecting the presence of proteins essential for the
 CC viability of a bacterial cell wall in samples such as cells, tissues,
 CC biological fluids, blood, serum, nose, ear or throat swabs with ligands,
 CC and for detecting corresponding target nucleic acid molecules with
 CC complementary sequences. The nucleic acids are also useful for
 CC determining whether a genomic nucleotide sequence of interest is
 CC essential for viability of a bacterial cell or whether it resides within
 CC an operon, by integrating an exogenous nucleotide sequence comprising a
 CC portion of an open reading frame of the genomic sequence of interest
 CC (comprising 200-500 base pairs) into the genomic sequence of interest
 CC which confers a selectable phenotype to the cell, and determining cell
 CC viability with a selection agent such as chloramphenicol. The nucleic
 CC acids and proteins are also useful as vaccines and for treating bacterial
 CC infections with gene therapy and antisense therapy. The nucleic acids
 CC also enable identification of targets suitable for the treatment of
 CC antibiotic resistant bacterial infections.

XX Sequence 243 AA;

Query Match 25.3%; Score 330.5; DB 22; Length 243;
 Best Local Similarity 34.7%; Pred. No. 3.2e-24;
 Matches 87; Conservative 38; Mismatches 103; Indels 23; Gaps 6;

QY 15 TTGGAGGGLATRERLYVGOGASAVLIDLPNSGGE-----AQAKKLGNNCFAPADVTSE 68
 DB 10 TTGSSSGIGLAIARHKAQAGANIVL-----NSRGAISEELAEPSNYGIRKVPISGDVSDF 65
 QY 69 KDVQTLALAKGKFGVDVAVNAGIYAVASKTYNKKGGTHTLEDQRYLVDNLMGTENV 128
 DB 66 ADPKRMIDQALIELSGVDVLYNNAGI--TQDTLMKKM-----TEADPEKYLKYNLGAFFNM 119
 QY 129 TRIVAGEMGNEPDGOGRGVITNTASVAFFEGVQAAYASASKGIVGNTPIARDLAP 188
 DB 120 TQSVL-----KPMKARREGAIIIMSSVYGLMGNIQANYAASKAGLIGFTSVAREVAS 173
 QY 189 IGRVMTIAPGLTGTPLTSLPEKVRNFLASQVPPFSRGLDPAEYAHLYQATIIENPFLNG 248
 DB 174 RNRVNVIAAPGMIESDMTALISDKIKETALQIPM-KFEGQAQVADLVFLAAGQYLNG 232
 QY 249 EVTRLDGAIKRM 259
 DB 233 QVVAIDGISM 243

RESULT 13

ID ABB54087 standard; Protein; 243 AA.

XX ABB54087;
 AC ABB54087;
 DT 16-MAY-2002 (first entry)
 XX
 DE Lactococcus lactis protein dabG1.
 KM Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
 OS Lactococcus lactis IL1403.
 XX
 PN FR2807446-A1.
 XX
 PD 12-OCT-2001.
 XX
 PF 11-APR-2000; 2000FR-0004630.
 XX
 PR 11-APR-2000; 2000FR-0004630.
 XX
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 XX
 PI Boletine A, Sorokine A, Renault P, Ehrlich SD;
 XX
 DR WPI; 2002-043418/06.
 XX
 PT New nucleotide sequence useful in the identification or Lactococcus

PT lactis and related species -
 PS
 XX Claim 6; SEQ ID No 789; 2504pp; French.

CC The present invention is related to a Lactococcus lactis nucleotide
 CC sequence (AB90521) and related proteins (AB93300-AB95621). The
 CC nucleic acid sequence is useful in the detection and/or amplification of
 CC nucleic acid sequence, particularly to identify Lactococcus lactis or
 CC related species. The proteins of the invention are useful for the
 CC biosynthesis or biodegradation of a composition of interest. The
 CC invention helps research in lactic bacteria, particularly useful in the
 CC production of yogurt and cheese.
 CC Note: The sequence data for this patent is based on equivalent patent
 CC WO20017334 (published 18-OCT-2001) which is available in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 243 AA;

Query Match 25.2%; Score 329.5; DB 23; Length 243;
 Best Local Similarity 31.7%; Pred. No. 4e-24;
 Matches 82; Conservative 49; Mismatches 103; Indels 25; Gaps 6;

QY 8 VKGLVAVITGGASGLIATARLYVGOGASAVLIDLPNSGGEQAQKL-----GNNCFV 60
 DB 3 IKNNKVFVGTGTRGIGKALIQFAKAGSNLII-----NGRGAISEELAEFTAYGVRVAVG 57
 QY 61 APADYTSKDVQTLALAKGKFGVDVAVNAGIYAVASKTYNKKGGTHTLEDQRYLVDY 120
 DB 58 ISGDISKEDAKQWVAEALITLGSVDILVNNAGI--TRDGSLKMS-----EDFESYKI 111
 QY 121 NLMGFNYIRLYVAGEMGNEPDGOGRGVITNTASVAFFEGVQAAYASASKGIVGNTL 180
 DB 112 NLTGAFNMTQAVL-----KMTTRARSGAIIIMSSVYGLMGNIQANYAASKAGLIGLTK 165
 QY 181 PIARDLAPIGIRVMTIAPGLTGTPLTSLPEKVRNFLASQVPPFSRGLDPAEYAHLYQAI 240
 DB 166 STAREVAAARNVAVNVAAGFIESDMEVLISDKVKDKMGQIIPM-KRFGMPREIATATQFL 224
 QY 241 IENPFLNGEVTRLDGAIKRM 259
 DB 225 ADEQYMTGQVLTIDGVSVM 243

RESULT 14

ID AAU35328 standard; Protein; 245 AA.

XX AAU35328;
 AC AAU35328;
 DT 14-FEB-2002 (first entry)
 XX
 DE Enterococcus faecalis cellular proliferation protein #615.
 KM Antisense; prokaryotic cellular proliferation protein;
 XX antibiotic; antibacterial; drug design.
 OS Enterococcus faecalis.
 XX
 PN WO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001MO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 XX
 PR 23-MAY-2000; 2000US-206848P.
 XX
 PR 26-MAY-2000; 2000US-207727P.
 XX
 PR 23-OCT-2000; 2000US-242578P.
 XX
 PR 27-NOV-2000; 2000US-253625P.
 XX
 PR 22-DEC-2000; 2000US-257931P.
 XX
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.

XX Hasselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
XX N-PSDB; AAS53187.

PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -

PS Example 3; Seq ID No 10921; 51pp; English.

XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 245 AA;

Query Match 24.8%; Score 323.5; DB 22; Length 245;
Best Local Similarity 33.7%; Pred. No. 1.6e-23;
Matches 84; Conservative 39; Mismatches 107; Indels 19; Gaps 5;

QY 15 ITGASGIGLATFARIVQGSAYLLD---LPSGGEAOKKXGNCVPAPADVTEKD 70
DB 10 ITGSTRGIGKAVALAFKAGNIVNGRSETTPORQETL--FGVCIGISGISPDFA 67
QY 71 VQTALALAKRGFGRVAVNCAIVASKYTNLKKGGTHLEDFRVLVDVNLMTFNVIR 130
DB 68 AGEMIAQATVDLGSIDILVNNAGIT-----NDKILLTMRKEDFNACIDIVLGTFFMTQ 121
QY 131 LVAGMGONEDDGGORVITNTASVAFEGVQVQQAASAKSGIYGTLPIDLP 190
DB 122 QAVKRMQO-----RSGRITINMASVSGLMGNVQQAATAASKAGVGTAKSAKEVAPRG 175
QY 191 IRVMTIAPGLTGTPLTLPLPEKVRNFTLASQVPPSPRLDPPPEYHVLVQAILTENPFLNGEV 250
DB 176 ITCNIAIAGFTIOTETDVLSEKVTQNMNAIPIQT-FQGVADVAATATFLAKSPYITGOV 234
QY 251 IRLDGAIRM 259
DB 235 VAVDGLVW 243

RESULT 15

AAU28344

AC AAU28344;

DT 18-DEC-2001 (first entry)

DE Novel human secretory protein, Seq ID No 701.

XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
XX ischaemia-reperfusion injury; haematopoiesis; cancer; neutrophil;
XX transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
XX amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;

KM ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
KM gut protection; lung; liver fibrosis; immune deficiency; infection;
KM severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
KM multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
KM fertility; analgesic; pain; antigen.

OS Homo sapiens.

PN WO200166689-A2.

PD 13-SEP-2001.

PS 05-MAR-2001; 2001WO-US04942.

PR 07-MAR-2000; 2000US-0519705.

PR 19-MAY-2000; 2000US-0574454.

PR 17-JUN-2000; 2000US-0596193.

PR 14-JUL-2000; 2000US-0616847.

PR 19-SEP-2000; 2000US-0665363.

PR 20-OCT-2000; 2000US-0693267.

PA (HYSE-) HYSEQ INC.

PI Tang YI, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

PI Zhao QA, Yang Y, Dymnac RT, Zhang J, Chen R, Xue AJ, Wang J;

DR WPI; 2001-589934/66.

DR N-PSDB; AAS45244.

PT Novel polypeptides and nucleic acids obtained from cDNA libraries

PT prepared from various human tissues, for diagnosis and treatment of

PT cancer, neurological, inflammatory, and autoimmune disorders -

XX Example 2; SEQ ID No 701; 107pp; English.

XX The invention relates to novel isolated human secreted polypeptides (I)
CC and polynucleotides (II). (I) and (II) are useful for treating
CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
CC involved in increasing haematopoiesis, stem cell survival, bone growth
CC and remodeling. (I), (II) and modulators of (II) are useful for
CC prophylaxis or treatment of one or more cancers. (II) is also useful for
CC creating transgenic animals useful for studying the in vivo activities of
CC the polypeptide as well as for studying modulators of the polypeptides.
CC (I) induces the proliferation of neural cells and regeneration of nerve
CC and brain tissue and is useful for the treatment of cerebral and
CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
CC activity, regulation of haematopoiesis and is useful for treating myeloid
CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
CC tissue growth, and in tissue repair, healing of burns, incisions,
CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
CC disorders, or periodontal disease. Furthermore, (I) is also useful for
CC gut protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, various immune deficiencies and
CC disorders including severe combined immunodeficiency (SCID), bacterial or
CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
CC reactions and conditions, such as asthma or other respiratory problems.
CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
CC fertility, metabolism, carbohydrate, anabolism, storage or elimination of
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
CC analgesic effects or other pain reducing effects, immunoglobulin like
CC activity and can act as an antigen in a vaccine composition to raise an
CC immune response. AAU28020-AAU28395 represent novel human secreted protein
XX amino acid sequences of the invention.

XX Sequence 257 AA;

Query Match 24.3%; Score 317; DB 22; Length 257;
Best Local Similarity 31.5%; Pred. No. 7.3e-23;

XX 02-APR-2001; 2001MO-US10720.
PF 31-MAR-2000; 2000US-193920P.
PR (MILL-) MILLENNIUM PHARM INC.
PA Meyers RA, Rudolph-Owen LA;
PI MPI; 2001-626438/72.
DR N-PSDB; AAT0573.
XX Novel isolated 21509 and 33770 polypeptides belonging to human
PT dehydrogenase family members, useful for treating cancer, diabetes,
PT atherosclerosis, glomerulonephritis, Crohn's disease, cirrhosis,
PT multiple sclerosis -
XX Claim 1(a); Fig 2; 14pp; English.

CC The present sequence is that of a novel human dehydrogenase,
CC designated 21509. The protein has a significant number of
CC structural characteristics in common with members of the
CC dehydrogenase/oxidoreductase family. Its expression pattern
CC suggests a role in tumour development. The invention provides
CC 21509 and 33770 nucleic acids, antisense molecules, recombinant
CC expression vectors, host cells and transgenic animals in which a
CC 21509 or 3370 gene has been introduced or disrupted. It also
CC provides 21509 and 33770 proteins, fusion proteins, antigenic
CC peptides and antibodies, and methods for screening for compounds
CC that modulate the expression or activity of 21509 or 33770
CC polypeptides or nucleic acids. Such modulators are used in methods
CC for inhibiting the proliferation or migration, or inducing the
CC killing, of 21509- or 33770-expressing cells, especially the
CC hyperproliferative and/or metastatic cells of a soft tissue tumour,
CC solid tumour or metastatic lesion, especially ovarian cancer, colon
CC cancer, lung cancer and liver cancer (claimed). Modulator
CC compounds are also used in claimed methods of modulating fatty acid
CC biosynthesis or retinoid biosynthesis in a cell. 21509 and 33770
CC nucleic acids can also be used to prepare diagnostic probes and in
CC gene (including antisense) therapy.

XX Sequence 237 AA:

Query Match 24.1%; Score 314; DB 22; Length 237;
Best Local Similarity 32.0%; Pred. No. 1.3e-22;
Matches 81; Conservative 41; Mismatches 105; Indels 26; Gaps 5;

QY 12 VAVITGASGIGLTAERLVGOGASAVILDPNSGGEAQAARKLNCCVPADVTSKDY 71
DB 4 VCAIFGSGRGIGRVAQAQMARKGYRLAIIARNLGGAAGAAGDGLHARSQVAKHVDV 63
QY 72 QALALAGKFGFRDVAVNCAGI-----AVASKTYNLKGGQTHLEDFOFVILNLTGTF 126
DB 64 QNTPEMKHLGRNFTLVNAGINRDSILVYRKT-----EDWQSLHNLGSM 112
QY 127 NVIRLVAGEMQNEPDGOGGQVITINASVAAPFGQQAAYASKSGIGVMTPIARDL 186
DB 113 LTCKAAMRAMIQ-----QGGSTVNWOSIVGLKNSQSYASASKGLVGFSPALKEV 166
QY 187 APIGIRVMTIAPGLGFTPLTSLPEKVRNFLASOVPPPSRLGDAEVAHLVQATITENPFL 246
DB 167 ARKRIRVNVVAPGFVHTMDKDEE---HLKKNITPL-GRGFIIVAHNAVIFLLESYI 222
QY 247 NGEVIRLDGAIRM 259
DB 223 TGHVLVVDGLOL 235

RESULT 18
AAB96397
ID AAB96397 standard; Protein; 241 AA.
XX
AC AAB96397;

XX 29-OCT-2001 (first entry)
DE Putative P. abyssi dehydrogenase #8.
XX Hyperthermophilic archaeon; hyperthermophilic protein.
XX Pyrococcus abyssi.
XX FR2792651-A1.
XX 27-OCT-2000.
XX 21-APR-1999; 99FR-0005034.
XX 21-APR-1999; 99FR-0005034.
XX 21-APR-1999; 99FR-0005034.
XX (CNRS) CNRS CENT NAT RECH SCI
XX (IFRE-) IFREMER INST FR RECH EXPL MER.
XX Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;
XX Querellou J, Weissenbach J, Saurin W, Heilig R;
XX MPI; 2001-126236/14.

PT New nucleotide sequences isolated from Pyrococcus abyssi encode
PT proteins useful in industry -
XX Claim 7; Pages 1087-1088; 1657pp; French.

CC The present invention relates to the genomic sequence of Pyrococcus
CC abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is
CC a hyperthermophilic archaeon, which is isolated from deep-sea
CC hydrothermal vents. The present invention has various potential industrial
CC uses, since the proteins are stable at very high temperatures, some up to
CC 110 degrees centigrade.
CC Note: This patent is in the same patent family as WO200065062, which
CC contains additional sequences as shown in AAB99132-AA999143,
CC AAH75903-AAH75920 and AAG64636.

XX Sequence 241 AA:

Query Match 23.9%; Score 312.5; DB 22; Length 241;
Best Local Similarity 34.1%; Pred. No. 1.9e-22;
Matches 87; Conservative 47; Mismatches 92; Indels 29; Gaps 7;

QY 8 VGVAVITGASGIGLTAERLVGOGASAVILDPNSGGEAQAARKLNCCVPADVTSKDY 60
DB 4 LKSKVALITGASGIGIRATAIELAKGVNVVINYSN---EBEAKTELCQGYVEITL 60
QY 61 APADVTSEKDVQATALALANGKGRVDVAVNCAGIAVASKTYNLKGGQTHLEDFOFVILN 120
DB 61 VKADVSNREVRVMAVKVIDKFGRIDILINNAGI--LGKT---KPLEVTDEMVRVLSV 115
QY 121 NMGTENVIRLVAGEMQNEPDGOGGQVITINASVAAPFGQQAAYASKSGIGVMTPIARDL 180
DB 116 NLNGAFTVQEVIRYI-----KKGKIVNASTAGKDGCTGVGHVYASKGGIATLTF 166
QY 181 PIARDLAPIGIRVMTIAPGLGFTPLTSLPEKVRNFLASOVPPPSRLGDAEVAHLVQAT 240
DB 167 NLARHLAP-NILVNAVAPGVDTDMLSSEKKE---MLKSLITGDIARPSEVAHAHVIPL 221
QY 241 IENPFLNGEYIRIDG 255
DB 222 LENDHTIGEVIDVNG 236

RESULT 19
AAU28156
ID AAU28156 standard; Protein; 237 AA.
XX
AC AAU28156;

XX 18-DEC-2001 (first entry)
XX Novel human secretory protein, Seq ID No 325.
XX Human: secreted protein; arthritis; Crohn's disease; sepsis; shock;
XX ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
XX transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
XX amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
XX ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
XX gut protection; lung; liver fibrosis; immune deficiency; infection;
XX severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
XX multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
XX fertility; analgesic; pain; antigen.
XX Homo sapiens.
XX WO200166689-A2.
XX 13-SEP-2001.
XX 05-MAR-2001; 2001WO-US04942.
XX 07-MAR-2000; 2000US-0519705.
XX 19-MAY-2000; 2000US-0574454.
XX 17-JUN-2000; 2000US-0596193.
XX 14-JUL-2000; 2000US-0616847.
XX 19-SEP-2000; 2000US-065363.
XX 20-OCT-2000; 2000US-0693267.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
XX Zhao QA, Yang Y, Dzmanac RT, Zhang J, Chen R, Xue AD, Wang J;
XX N-PSDB; AA645056.
XX WPI: 2001-569934/66.
XX Novel polypeptides and nucleic acids obtained from cDNA libraries
XX prepared from various human tissues, for diagnosis and treatment of
XX cancer, neurological, inflammatory, and autoimmune disorders -
XX Example 4; SEQ ID No 325; 107pp; English.
XX The invention relates to novel isolated human secreted polypeptides (I)
XX and polynucleotides (II). (I) and (II) are useful for treating
XX inflammatory conditions such as arthritis, nephritis, Crohn's disease,
XX ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
XX involved in increasing haematopoiesis, stem cell survival, bone growth
XX and remodeling. (I), (II) and modulators of (II) are useful for
XX prophylaxis or treatment of one or more cancers. (II) is also useful for
XX creating transgenic animals useful for studying the in vivo activities of
XX the polypeptide as well as for studying modulators of the polypeptides.
XX (I) induces the proliferation of neural cells and regeneration of nerve
XX and brain tissue and is useful for the treatment of central and
XX peripheral nervous system diseases and neuropathies, such as Alzheimer's,
XX Parkinson's disease, Huntington's disease, and amyotrophic lateral
XX sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
XX activity, regulation of haematopoiesis and is useful for treating myeloid
XX or lymphoid cell disorders, platelet disorders such as thrombocytopenia
XX and for regeneration of bone, cartilage, tendon, ligament and/or nerve
XX tissue growth, and in tissue repair, healing of burns, incisions,
XX ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
XX disorders, or periodontal disease. Furthermore, (I) is also useful for
XX gut protection or regeneration and treatment of lung or liver fibrosis,
XX reperfusion injury in various tissues, various immune deficiencies and
XX disorders including severe combined immunodeficiency (SCID), bacterial or
XX fungal infections, autoimmune disorders e.g. multiple sclerosis,
XX rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
XX reactions and conditions, such as asthma or other respiratory problems.
XX In addition, (I) affects biorhythms or circadian cycles of rhythms,
XX fertility, metabolism, catabolism, anabolism, storage or elimination of
XX lipid, protein, carbohydrate, vitamins, minerals, provides

CC analgesic effects or other pain reducing effects, immunoglobulin like
CC activity and can act as an antigen in a vaccine composition to raise an
CC immune response. AAU28020-AAU28395 represent novel human secreted protein
CC amino acid sequences of the invention.
XX
XX Sequence 237 AA;
XX
XX Query Match 23.9%; Score 312; DB 22; Length 237;
XX Best Local Similarity 31.6%; Pred. No. 2e-22;
XX Matches 80; Conservative 42; Mismatches 105; Indels 26; Gaps 5;
XX
QY 12 VAVITGASGLGATLRLVGGASAVLDPNSGGEAAKKLGNVCVAPADYSEKDY 71
DB 4 VCAVFGSGSRGIGRAVAQLAKARKGYRLAVIARNLEGAKAAAGDGGDHLAFSCDVAKEDV 63
QY 72 QTALALAKGKFGVDVAVNCAGI-----AVASKTYNLKKGQRTLEDFOFVLDVNLGTF 126
DB 64 QNTPEEMKHLGKYNFLVNAAGINRGDLVRTT-----EDMYSQLHTNLGSM 112
QY 127 NVIRLVAGENGQNEPDGGGQGVIIINTASYAAFEQVGGQANASASKGIYGMTLPAROL 186
DB 113 LTCKAAARTMIQO-----OGGSIYVNGSIVGLKNGSGQSVASKSGLVGFSRALAKEV 166
QY 187 APTGIRYMTIAPGLFGPRLTSLPEKVRNPLASQVFPSPRLGDPAYAHVQAIIENPFL 246
DB 167 ARKRTIRNVVAPGPHVHTDKRLKEE---HLKKNIPL-GHFGETIVAHAVVFLLESPI 222
QY 247 NGEVIRLDGAI RM 259
DB 223 TGHVLYVDGGIQL 235
XX
XX RESULT 20
XX AAB19928
XX ID AAB19928 standard; Protein: 237 AA.
XX
XX AAB19928;
XX
XX DT 19-MAR-2001 (first entry)
XX
XX DE Human oxidoreductase OXRD-3.
XX
XX KW OXRD-3; human; oxidoreductase; dehydrogenase; cell proliferation;
XX neurological disease; smooth muscle disease; autoimmune disease;
XX inflammation; antiproliferative; neuroprotective;
XX immunosuppressive; antiinflammatory; therapy; diagnosis.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 66 /note= "O-phosphorylated"
XX FT Misc-difference 95 /note= "O-phosphorylated"
XX FT Misc-difference 114 /note= "O-phosphorylated"
XX FT FT /note= "O-phosphorylated"
XX FT Region 3..184 /note= "short-chain dehydrogenase signature"
XX
XX PN WO200071679-A2.
XX
XX PD 30-NOV-2000.
XX
XX PF 19-MAY-2000; 2000WO-US13879.
XX
XX PR 20-MAY-1999; 99US-0135049.
XX PR 27-MAY-1999; 99US-0136740.
XX
XX PA (INCY-) INCYTE GENOMICS INC.
XX
XX PI Yue H, Tang YT, Baughn MR, Lu DAM;
XX
XX WPI: 2001-025146/03

DR N-PSDB; AAA89187.
 XX New human oxidoreductase proteins useful for diagnosing, treating or
 PT preventing proliferative, neurological, genetic, smooth muscle,
 PT autoimmune or inflammatory disorders associated with abnormal
 PT expression of oxidoreductase proteins -
 XX
 PS Claim 1(a): Page 83; 95pp; English.
 XX
 CC The present sequence is that of human oxidoreductase OXR-3, as
 CC deduced from a cDNA clone (see AAA89187) isolated from a lung tumour
 CC cDNA library. The protein shows homology to Escherichia coli
 CC 3-oxoacyl-(acyl)-carrier protein, and includes a short-chain
 CC dehydrogenase signature. OXR-3 is expressed in nervous, reproductive,
 CC cardiovascular and gastrointestinal tissue, and may be involved in
 CC cell proliferation and inflammation. The invention provides OXR-1
 CC to -8 polypeptides (see AAB1926-33) and polynucleotides (see
 CC AAA89185-92). It also provides methods for using these polypeptides
 CC and polynucleotides for diagnosing, treating or preventing disorders
 CC associated with expression of OXR, especially cell proliferative,
 CC neurological, genetic, smooth muscle, and autoimmune/inflammatory
 CC disorders. The proteins can also be used to screen for agonists
 CC and antagonists useful for treating these conditions, while
 CC antibodies that bind to OXR may be used for diagnosis or in assays
 CC to monitor patient treatment.
 XX
 SQ Sequence 237 AA;
 Query Match 23.9%; Score 312; DB 22; Length 237;
 Best Local Similarity 31.6%; Pred. No. 2e-22;
 Matches 80; Conservative 42; Mismatches 105; Indels 26; Gaps 5;
 OY 12 VAVITGGASGIGLTAERLVQGSASAVLDLPNSGGEAQAQKLGNNCFAPADVTSEKDV 71
 DB 4 VCAVFGSGSRGGRVADLMARKGRVLAIVARNEGAKAAAGDGGDLASCDAVAKHDV 63
 OY 72 QFALALAKGKGRVDVAVNCAGT-----AVASKTYNKKQOTHTLEDFOVLVNNMGRT 126
 DB 64 QNFEEMERKHLGRNPLFNAGINRDLVTRKT-----EDMVSQLTNTLLGSM 112
 OY 127 NVIRLVAGMGONPEPDGQGRVITNTASVAFAEGVGAAYASAKSGIGMTLPJARDL 186
 DB 113 LTCAARMTMQ-----QGGSIVNVSIGLKGSGSVYSASKGLVGFBSALAKV 166
 OY 187 APGIRVKTAPGIFGPIPLTSLPEKVRNPLASGVPPSRIGDPAEVAHLYQALIEPPL 246
 DB 167 ARKIRVNVVAPRGVHDMTKDLKE--HLKNKIPL-GRFGTIEVAHAHVFLLESPYI 222
 OY 247 NGEVIRLDGAIRM 259
 DB 223 TGHVLYVDGGLQ 235
 RESULT 21
 ID AAY95746 standard; Protein: 247 AA.
 XX
 AC AAY95746;
 XX
 DT 25-OCT-2000 (first entry)
 XX
 DE Bacillus megaterium 3-keto-acyl-CoA reductase Phab.
 XX
 KM Polyhydroxyalkanoate; polyhydroxybutyrate; transgenic plant; Phab;
 XX 3-keto-acyl-CoA reductase.
 XX
 OS Bacillus megaterium.
 XX
 PN WO20040730-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 07-JAN-2000; 2000WO-US00364.

XX
 PR 07-JAN-1999; 9905-0115592.
 XX
 PA (UYMA-) UNIV MASSACHUSETTS.
 XX
 PI Cannon MC, Cannon FC, Mccool GJ, Valentini HE, Gruys KJ;
 XX
 DR WPI: 2000-532624/48.
 XX
 DR N-PSDB; AAA50142.
 XX
 PT New nucleic acid fragment encoding proteins involved in
 PT polyhydroxyalkanoate (PHA) biosynthesis, useful in the production of
 PT transgenic plants or recombinant plant cells which can express PHAs
 PT such as polyhydroxybutyrate -
 XX
 PS Claim 85; Page 137-138; 153pp; English.
 XX
 CC The present sequence is that of Phab, a 3-keto-acyl-CoA-reductase
 CC protein of Bacillus megaterium. The sequence was deduced from an
 CC open reading frame identified in an isolated 7,916 bp fragment of
 CC B. megaterium strain 11561 genomic DNA (see AAA50142). The 7,916 bp
 CC DNA fragment includes genes encoding proteins (see AAY95743-47)
 CC involved in polyhydroxyalkanoate (PHA) biosynthesis. Nucleic acids
 CC encoding these proteins are useful for creating transgenic plants or
 CC recombinant host cells which have the capability of expressing PHAs
 CC such as polyhydroxybutyrate, polyhydroxyvalerate,
 CC polyhydroxyhexanoate, polyhydroxyoctanoate, polyhydroxydecanoate or
 CC their copolymers. Claimed methods for preparing a PHA involve
 CC obtaining a plant or a cell comprising a nucleic acid encoding
 CC a 3-keto-acyl-CoA reductase (especially the present sequence), and
 CC a nucleic acid encoding a PHA synthase (see AAY95747), and growing
 CC the plant or cell under conditions suitable for PHA production.
 XX
 SQ Sequence 247 AA;
 Query Match 23.7%; Score 309; DB 21; Length 247;
 Best Local Similarity 29.5%; Pred. No. 4.2e-22;
 Matches 79; Conservative 59; Mismatches 92; Indels 38; Gaps 9;
 OY 7 SVKGLVAVITGGASGIGLTAERLVQG-----ASAVLDLPNSGGEAQAQK 53
 DB 3 TLOGKVAIYTGSGSKGAITRELASNGKVAVNTSSKESAEAVKIKONGGSA---- 58
 OY 54 LGNNCFAPADVTSEKDVQGTALALAKGKGRVDVAVNCAGIVASKTYNKKR-GQTHLE 112
 DB 59 -----IADVADVSYYDQAKHLIEETRAAFGQDITLNNAGT---TRDSFKKLG- 106
 OY 113 DFQVRLVNNMGTFNVIRLVAGMGONPEPDGQGRVITNTASVAFAEGVGAAYASAK 172
 DB 107 DMKRVIDVNLHVSYNTSALTHLESE--GGR--VINISSIIGQAGGFGQTYSAK 160
 OY 173 GGIYGMTLPIDARDAPIGIRVMTIAPGLETPPLTSLPEKVRNPLASGVPPSRIGDPAE 232
 DB 161 AGMLGFTKSLALELATGTAVNAICPGFETEMVAPEDVAKIYAKIP-TRRLGHAE 219
 OY 233 YAH-LVQAIENPFNGEVIIRLDGAIRM 259
 DB 220 IARGVVYLANKGAVITRQQLNINGLHYM 247
 RESULT 22
 ID ABB48892 standard; Protein: 247 AA.
 XX
 AC ABB48892;
 XX
 DT 05-FEB-2002 (first entry)
 XX
 DE Listeria monocytogenes protein #1596.
 XX
 KM Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 XX vitamin B12; bacterial infection; disease.
 XX

OS Listeria monocytogenes.
 PN WO200177335-A2.
 XX 18-OCT-2001.
 PD 11-APR-2001; 2001WO-FR01118.
 XX 11-APR-2000; 2000FR-0004629.
 PR (INSP) INST PASTEUR.
 XX Buchrieser C, Fraigneul L, Couve E, Rusniok C, Fsihi H, Dehoux P,
 PI Dussanquet O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P,
 PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA,
 PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A,
 PI Chakraborty T, Dammann E, Hain T, Berche P, Chardot A, Durant L,
 PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N,
 PI Madueno E, De Pablos B, Wehland J, Kaerst U, Entian K, Hant J,
 PI Rose M, Voss H;
 DR WPI; 2002-010914/01.
 XX
 PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
 PT and prevention of Listeria and related bacterial infections, and
 PT related polypeptides
 PS Claim 6; SEQ ID No 1597; 192pp; French.
 XX
 CC The present invention relates to the genome sequence of Listeria
 CC monocytogenes EGD-e (see AB03041). The genome sequence and fragments of
 CC it are useful for selecting probes and primers for detecting genes in L.
 CC monocytogenes and related organisms, and for studying genetic
 CC polymorphisms and other genomes. The present sequence is a protein
 CC encoded by the genome sequence of the present invention. Proteins
 CC expressed from the genome sequence are useful for raising specific
 CC antibodies, identification of L. monocytogenes and related organisms, and
 CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
 CC B12. The genome sequence and proteins encoded by it are also useful for
 CC selecting compounds that regulate gene expression and cell replication
 CC and modulate L. monocytogenes-related diseases. In addition, the genome
 CC sequence and proteins encoded by it are useful in pharmaceutical and
 CC vaccines compositions for the treatment or prevention of infections by L.
 CC monocytogenes and related organisms.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 SQ Sequence 247 AA;
 XX
 Query Match 23.68; Score 308.5; DB 23; Length 247;
 Best Local Similarity 32.08; Pred. No. 4,7e-22;
 Matches 85; Conservative 46; Mismatches 102; Indels 33; Gaps 7;
 QY 7 SVKGLAVITGGASGIGLATLAERLVGQASAVLDDLPNSGGEAQA---KRL---GNNC 58
 DB 2 TLOGKAVAVVGGSGIGRIDIAINLAKGANIFF---NYNGSPEAEETAKLVAEGVEV 57
 QY 59 VFPAADVTSEKDVOTALAKKRGFRVDVAVNCAGTAVASKTNYLNKGGHTLEDQRYL 118
 DB 58 EAKKANAVALAEDDAFAKQALIERGRGDIIVNNAIGTRDMLRMKE-----DEMDVY 111
 QY 119 DVNLMTGFNVTRLVAGMGQNEPDQSGORCVITNTASVAEFEGQGAAYSASKGIIVGM 178
 DB 112 NINIKGFTLCTKAVSRFMKQ-----RASKIIMASVOLLIGNAGQANYVASKAGVIGL 165
 QY 179 TLTPARLAPLGIKIVMTIAPGLRGTPLLTSIPEKVRNFIASQVPEPRLGDPREYALVQ 238
 DB 166 TKTTARELAPRGIVNNAVAPGFTITDMDTKLIDETKRAMLAQIP-----LANYGTEDIAN 221
 QY 239 AII-----ENFNLGEVIRLDGARIM 259
 DB 222 AVFLASDASKYITGRTLSVDGGMV 247

RESULT 23
 AAU28296
 ID AAU28296 standard; Protein: 288 AA.
 XX
 AC AAU28296;
 XX
 DE 18-DEC-2001 (first entry)
 DE
 DE Novel human secretory protein, Seq ID No 653.
 XX
 KM Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KM ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KM transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KM amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KM ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KM gut protection; lung; liver fibrosis; immune deficiency; infection;
 KM severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KM multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KM fertility; analgesic; pain; antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200166689-A2.
 XX 13-SEP-2001.
 PD 05-MAR-2001; 2001WO-US04942.
 XX
 PF 07-MAR-2000; 2000US-0519705.
 XX 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0663563.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Dimañac RT, Zhang J, Chen R, Xue AD, Wang J;
 XX
 DR WPI; 2001-589934/66.
 DR N-PSDB; AAS45196.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders
 PT
 XX
 XX Example 2; SEQ ID No 653; 107pp; English.
 XX
 CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and

disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (1) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein amino acid sequences of the invention.

Sequence 288 AA:

Query Match 23.0%; Score 300.5; DB 22; Length 288;
Best Local Similarity 29.9%; Pred. No. 3.6e-21;
Matches 84; Conservative 44; Mismatches 110; Indels 43; Gaps 6;

1 MAACRSVKGIVAVITGGASGLTAETRLVGGASAVLLDLPNSGGEAOKKGNVCVF 60
10 MATGTR-YAGKVAVVITGGRGIGAGIYRAVNSGARVYICDKDSGRALGELPGGCL 68
QY 61 APADVTSEKDVQATLALAKGFEGRVDVAVNCAGIAVASKTYNLKGGOTHTLEDFORVLDV 120
DB 69 SFCDVTQEDVDVKILVSETIRFRGLDCVNNAGHPP-----QRPETSAHGFRLLEL 123
QY 121 NLKGTFFVIRLVAGEMONEPDGCGRGVITNTASVAEFGVGOAAYASAKGIVMTL 180
DB 124 NLGTYITLTKALPYLRKSQ-----GVNINISLVGAIGQAQAVYVAITKGAIVAMRK 176
QY 181 PIADLAPIGIRVMTIAPGLFPLTSLPEKYANFLASQVPP----- 224
DB 177 ALADESPYGVAVNCISPGNIMTLMEE-----LAALMPDPRAITREGMLAQGRSV 228
QY 225 -----SRLGDPAEY-AHLVCAITENPFLNGEVIRLDGAIRM 259
DB 229 QIQPLGRMGPAVEGAANAVFLASDANCTGIXLIVTGAE 269

RESULT 24

AAV54421
ID AAV54421 standard; Protein: 244 AA.

AC AAV54421;

DT 06-APR-2000 (first entry)

DE Amino acid sequence of a beta-ketoacyl-ACP reductase enzyme.

KW Beta-ketoacyl-ACP reductase: Type II fatty acid synthetase;

KM stereoselectivity: 4-chloroacetoacetic acid ester;

KM (S)-4-halo-3-hydroxybutyric acid ester; 4-halo-acetoacetic acid ester;

KM beta-ketoacyl-acyl carrier protein reductase; acetoacetyl-CoA reductase;

KM polybeta-hydroxy fatty acid biosynthesis; optically active;

4-halo-3-hydroxybutyric acid ester.

XX Escherichia coli.

EP955375-A2.

PD 10-NOV-1999.

PF 10-MAY-1999; 99EP-0109403.

PR 08-MAY-1998; 98JP-0126507.

PR 21-OCT-1998; 98JP-0300178.

PR 05-APR-1999; 99JP-0098205.

PA (DAIL) DAICEL CHEM IND LTD.

PI Yamamoto H;

WPI; 2000-118183/11.

DR N-PSDB; AA245746.

PT Producing optically pure (S)-4-halo-3-hydroxybutyric acid ester -

PS Claim 3; Page 16-17; 34pp; English.

The present sequence represents a beta-ketoacyl-ACP reductase protein of *Escherichia coli*. The beta-ketoacyl-ACP reductase enzyme constitutes a type II fatty acid synthetase. The enzyme has an extremely high reducing activity and stereoselectivity towards 4-chloroacetoacetic acid ester. The specification describes a method for producing a (S)-4-halo-3-hydroxybutyric acid ester. The method comprises asymmetrically reducing 4-halo-acetoacetic acid ester or its derivative with beta-ketoacyl-acyl carrier protein reductase constituting Type II fatty acid synthase, or acetoacetyl-CoA reductase constituting the polybeta-hydroxy fatty acid biosynthesis system. The novel method is used to produce optically active 4-halo-3-hydroxybutyric acid ester, with a high purity.

Sequence 244 AA:

Query Match 22.8%; Score 297.5; DB 21; Length 244;
Best Local Similarity 30.4%; Pred. No. 5.6e-21;
Matches 77; Conservative 50; Mismatches 111; Indels 15; Gaps 4;

9 KGLVAVITGGASGLTAETRLVGGASAVLLDLPNSGGEAOKKGNVCVFAPADVTSE 68
DB 4 EGKIALVITGASRGIGRAIETLARGARVIGTSENQAQALSDYLGANGKGLMLNVTDP 63
QY 69 KDQVATLALAKGFEGRVDVAVNCAGIAVASKTYNLKGGOTHTLEDFORVLDNLKGTENV 128
DB 64 ASIESVLEKIRAEFGVDLTVNNAIGTRNLMRKD-----EDMNDIETNLSVPRL 117
QY 129 IRLVAGEMONEPDGCGRGVITNTASVAEFGVGOAAYASAKGIVMTLPIARDLAP 188
DB 118 SKAVRAMMKK-----RHGRITITIGSVYGTINGNGOANVAAKAGLIGFSKSLAREVAS 171
QY 189 IGRVMTIAPGLFPLTSLPEKYANFLASQVPPSRLGDPAEYAHLYO--AITENPFL 246
DB 172 RGITVAVVAPDGFLETMTALSDDORAGITLQVP-AGRLGAGQELANNVAFASDPAEYAI 230

QY 247 NGEVIRLDGAIRM 259

DB 231 TGETLHVNGMYM 243

RESULT 25

AAU34533
ID AAU34533 standard; Protein: 244 AA.

AC AAU34533;

DT 14-FEB-2002 (first entry)

DE E. coli cellular proliferation protein #114.

KW Antisense; prokaryotic cellular proliferation protein;

KW antibiotic; antibacterial; drug design.

XX Escherichia coli.

WO200170955-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US09180.

PR 21-MAR-2000; 2000US-191078P.

PR 26-MAY-2000; 2000US-206848P.

PR 23-OCT-2000; 2000US-207727P.

PR 27-NOV-2000; 2000US-242578P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX
XX Haeselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GT,
PI Yamamoto RT, Xu HH;
PI WPI; 2001-611495/70.
DR N-PSDB; AAS52392.
XX
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX
PS Example 3; Seq ID No 10126; 51pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 244 AA:
Query Match 22.8%; Score 297.5; DB 22; Length 244;
Best Local Similarity 30.4%; Pred. No. 5.6e-21;
Matches 77; Conservative 50; Mismatches 11; Indels 15; Gaps 4;
OY 9 KGLVAVITGGASGLGATATERTVGGASAVLLDLPNSGGEAOKLGNVCVFAPADVTSE 68
DB 4 EGRKIALVTGASRGIGRATAETLAETLAAGAVTGTATSENGCAISDYLGANGKGLMNTDP 63
OY 65 KDVOTRALALAKGKFRVDVAVNACIAVASKTYNKKGQTHLEDFOFVLDVNLMTFFNV 128
DB 64 ASIESYLERIRAFEFVEDILVNNAGITDNLIMRKD-----EEMNDIETNLSVFERL 117
OY 129 IRLVAGEMGQNPDDGGQGVIIINTASVAFAFGQVQAAYSASKGIYGMTLPYADLAP 188
DB 118 SKAVYRAMMK-----HGRITITGSYVGTMGNGQANVAAKAGLIGFSKSLAREVAS 171
OY 189 IGIRVYTTAPGLFGTPLLTSLEPKYKRNFLASQVPPPSRLGDPAEYAHVQ--ATLENPFL 246
DB 172 RGIITVNVVAPGFIETDMTRALSDDGRAIGLQVP-AGRLGGAQETANNAVAFLASDEAYI 230
OY 247 NGEVIRLDGAIRM 259
DB 231 TGSETLHVNGMYM 243

Search completed: June 23, 2003, 14:28:26
Job time : 42.6667 secs

Thu Jun 26 06:55:09 2003

us-09-931-186-4.rspt

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 14:22:37 ; Search time 31.6667 Seconds
(without alignments)
1698.262 Million cell updates/sec

Title: US-09-931-186-4
Perfect score: 1304
Sequence: 1 MAAVRSYKGLVAVITGAS.....ENPLNGEVIRLDGAIKMP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1240.5	95.1	252	4	Q96HDS
2	1162	89.1	261	11	Q96HNS
3	1158	88.8	261	11	Q96HNS
4	993	76.2	196	4	Q8TCV9
5	750	57.5	258	5	Q19102
6	720	55.2	255	16	Q910T0
7	711	54.5	255	16	Q8VBS0
8	689.5	52.9	252	16	Q8XWEO
9	671.5	51.5	250	16	Q8E544
10	670	51.4	255	16	Q92T81
11	667	51.2	253	16	Q96HMD
12	652	50.0	255	2	Q9AHY1
13	642	49.2	257	16	Q8UFI2
14	607	46.5	126	11	Q9DCX5
15	603.5	46.3	264	5	Q8T2L7
16	595	45.6	260	16	Q9ABU6

17	386	29.6	443	2	Q935J3	Q935J3 myxococcus
18	373.5	28.6	246	16	Q8X1H1	Q8X1H1 clostridium
19	355.5	27.3	244	16	Q89YD6	Q89YD6 streptococ
20	355	27.2	242	16	Q9HW15	Q9HW15 pseudomonas
21	343.5	26.3	249	16	Q97DA6	Q97DA6 clostridium
22	337.5	25.9	247	16	Q8R9W0	Q8R9W0 thermococcus
23	336.5	25.8	297	3	Q42774	Q42774 neurospora
24	333.5	25.6	246	16	Q9KA03	Q9KA03 bacillus ha
25	333.5	25.6	251	16	Q8VYD0	Q8VYD0 anabaena sp
26	332	25.5	246	16	Q8F636	Q8F636 bacillus ha
27	326.5	25.0	248	2	Q9KJF1	Q9KJF1 thauera aro
28	325.5	25.0	243	16	Q9FBC3	Q9FBC3 streptococ
29	324.5	24.9	243	16	Q9CFH7	Q9CFH7 lactococcus
30	323.5	24.8	260	4	Q96KK9	Q96KK9 homo sapien
31	323	24.8	261	13	Q8UUM4	Q8UUM4 oryzias lat
32	322	24.7	271	10	Q94G09	Q94G09 cucumis sat
33	322	24.7	262	2	Q91G98	Q91G98 streptomyce
34	321	24.6	263	16	Q9K1M4	Q9K1M4 streptomyce
35	320	24.5	261	6	Q8WMD4	Q8WMD4 macaca mula
36	320	24.5	271	10	Q94G10	Q94G10 cucumis sat
37	317.5	24.3	246	2	Q9EX74	Q9EX74 rhodococcus
38	317	24.3	299	17	Q97UK6	Q97UK6 sulfolobus
39	315.5	24.2	260	16	Q88068	Q88068 streptomyce
40	315	24.2	267	10	P93697	P93697 vicia ungu
41	314.5	24.1	259	16	Q8U616	Q8U616 agrobacteri
42	313.5	24.0	240	17	Q90F54	Q90F54 pyrococcus
43	313	24.0	258	2	Q9F8V0	Q9F8V0 streptomyce
44	312.5	24.0	296	16	Q9ABX6	Q9ABX6 caulobacter
45	312.5	24.0	313	2	Q93H00	Q93H00 streptomyce
46	312	23.9	237	4	Q8MTW8	Q8MTW8 homo sapien
47	311.5	23.9	249	2	Q9A7T2	Q9A7T2 thauera aro
48	311	23.8	247	16	Q8PRT6	Q8PRT6 xyella fas
49	311	23.8	244	16	Q8YD94	Q8YD94 brucella me
50	309.5	23.7	244	16	Q8ZFT5	Q8ZFT5 yeastina pe
51	309	23.7	253	16	Q8U759	Q8U759 agrobacteri
52	306	23.5	256	16	Q8ZB06	Q8ZB06 yeastina pe
53	303.5	23.3	236	11	Q91VT4	Q91VT4 mus musculu
54	303.5	23.3	247	16	Q8Y690	Q8Y690 listeria mo
55	302.5	23.2	248	16	Q8U9B5	Q8U9B5 agrobacteri
56	302.5	23.2	249	2	Q8LBS5	Q8LBS5 geobacillus
57	302	23.2	263	2	Q9SSE7	Q9SSE7 streptomyce
58	302	23.2	273	2	Q9F501	Q9F501 streptomyce
59	301.5	23.1	247	16	Q92AK1	Q92AK1 listeria in
60	301.5	23.1	260	17	Q8U3B3	Q8U3B3 pyrococcus
61	301	23.1	247	2	Q9ZFP3	Q9ZFP3 bacillus me
62	300.5	23.0	296	5	Q9XX28	Q9XX28 caenorhabdi
63	300	23.0	250	2	Q56840	Q56840 xanthobacte
64	298	22.9	252	17	Q970D4	Q970D4 sulfolobus
65	297.5	22.8	254	16	Q92PP8	Q92PP8 rhizobium m
66	296.5	22.7	258	16	Q33339	Q33339 mycobacteri
67	296.5	22.7	538	2	Q8VMT5	Q8VMT5 rhizobium s
68	296	22.7	245	16	Q8YD01	Q8YD01 brucella me
69	296	22.7	315	10	Q949M3	Q949M3 brassica na
70	296	22.7	320	10	Q93X62	Q93X62 brassica na
71	295	22.6	360	16	Q9FRT1	Q9FRT1 streptomyce
72	295	22.6	328	10	Q93X67	Q93X67 brassica na
73	294	22.5	255	17	Q9HQ41	Q9HQ41 halobacteri
74	294	22.5	265	16	Q9S2E4	Q9S2E4 streptomyce
75	293.5	22.5	267	2	Q9LBS2	Q9LBS2 listeria a
76	291.5	22.4	254	10	Q949M2	Q949M2 brassica na
77	291.5	22.4	270	4	Q9BPK1	Q9BPK1 homo sapien
78	291.5	22.4	270	4	Q9BPK1	Q9BPK1 homo sapien
79	291	22.3	246	2	Q33HB3	Q33HB3 streptomyce
80	291	22.3	255	16	Q8R0D3	Q8R0D3 thermococ
81	291	22.3	258	16	Q930L5	Q930L5 rhizobium m
82	290	22.2	272	16	Q8YH00	Q8YH00 brucella me
83	289.5	22.2	405	16	Q98A50	Q98A50 rhizobium l
84	289	22.2	243	16	Q8RC25	Q8RC25 fuscobacteri
85	287.5	22.0	247	2	Q930F0	Q930F0 azotobacter
86	287.5	22.0	303	10	Q9SC00	Q9SC00 arabidopsis
87	287	22.0	317	10	Q93X68	Q93X68 brassica na
88	286.5	22.0	244	16	Q8X815	Q8X815 escherichia
89	286.5	22.0	245	16	Q8R0H9	Q8R0H9 thermococ

ALIGNMENTS

```

90 286.5 22.0 246 2 Q9RB80 Q9RB80 burkholderi
91 285.5 21.9 254 16 Q9RT26 Q9RT26 deinoxococcus
92 285 21.9 255 16 Q9PCQ2 Q9PCQ2 xyliella fas
93 284.5 21.8 246 2 Q9F519 Q9F519 streptomyc
94 284.5 21.8 257 16 Q9WYD3 Q9WYD3 thermotoga
95 284 21.8 256 17 Q8RTU5 Q8RTU5 methanosarc
96 283.5 21.7 253 16 Q8CH41 Q8CH41 lactococcus
97 283.5 21.7 272 16 Q9RGL1 Q9RGL1 staphylococ
98 283 21.7 252 16 Q92PPO Q92PPO rhizobium m
99 283 21.7 275 16 Q9K4H0 Q9K4H0 streptomyc
100 282.5 21.7 521 16 Q9A7A9 Q9A7A9 caulobacter

```

```

RESULT 1
Q96HD5 PRELIMINARY; PRT; 252 AA.

```

```

AC 096HD5:
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
DE Similar to hydroxyacyl-coenzyme A dehydrogenase, type II.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRNIN;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL: BC008708; AA08708.1; -.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 252 AA; 25984 MW; F36BB71070CE872D CRC64;

```

```

Query Match 95.1%; Score 1240.5; DB 4; Length 252;
Best Local Similarity 96.2%; Pred. No. 4.4e-78;
Matches 251; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

```

```

QY 1 MAAAVRSKGLVAVITGASGLGATAEKLVGGASAVLLDLPNSGGEAOKKLGNNVF 60
DB 1 MAAACRSVKGLVAVITGASGLGATAEKLVGGASAVLLDLPNSGGEAOKKLGNNVF 60
QY 61 APADVTSEKDYQYALAKKFKGRVDVAVNCAGIAVASKTYNKKGOTHTLEDFORVLDV 120
DB 61 APADVTSEKDYQYALAKKFKGRVDVAVNCAGIAVASKTYNKKGOTHTLEDFORVLDV 120
QY 121 NLKGTFFVIRLVAGMGQNEPDGQGRVITINTASVAEFEGYQQAAYSASKGIYGMTL 180
DB 121 NLKGTFFVIRLVAGMGQNEPDGQGRVITINTASVAEFEGYQQAAYSASKGIYGMTL 180
QY 181 PIADLAPIGIRVMTIAGLFTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHLYQAI 240
DB 181 PIADLAPIGIRVMTIAGLFTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIRLDGAIKMP 261
DB 241 IENPFLNGEVIRLDGAIKMP 261
QY 232 IENPFLNGEVIRLDGAIKMP 252
DB 232 IENPFLNGEVIRLDGAIKMP 252

```

```

RESULT 2
Q99N15 PRELIMINARY; PRT; 261 AA.
AC 099N15:
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)

```

```

DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Short chain L-3-hydroxyacyl-CoA dehydrogenase.
GN HSD17B10 OR SCHAD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. Pubmed=11165016;
RX MEDLINE=21095701; Pubmed=11165016;
RA He X.Y., Merz G., Chu C.H., Lin D., Yang Y.Z., Mehta P., Schulz H.,
RA Yang S.Y.;
RT "Molecular cloning, modeling, and localization of rat type 10 17beta-
RT hydroxysteroid dehydrogenase."
RL Mol. Cell. Endocrinol. 171:89-98(2001).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL: AF233685; AA015008.1; -.
DR HSSP: AF0351; 166W.
DR MGD: MGI:1333871; Hsd17b10.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 261 AA; 27273 MW; F371ED8A15CFEFAF CRC64;

```

```

Query Match 89.1%; Score 1162; DB 11; Length 261;
Best Local Similarity 88.1%; Pred. No. 1.2e-72;
Matches 230; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

```

```

QY 1 MAAAVRSKGLVAVITGASGLGATAEKLVGGASAVLLDLPNSGGEAOKKLGNNVF 60
DB 1 MAAACRSVKGLVAVITGASGLGATAEKLVGGASAVLLDLPNSGGEAOKKLGNNVF 60
QY 61 APADVTSEKDYQYALAKKFKGRVDVAVNCAGIAVASKTYNKKGOTHTLEDFORVLDV 120
DB 61 APADVTSEKDYQYALAKKFKGRVDVAVNCAGIAVASKTYNKKGOTHTLEDFORVLDV 120
QY 121 NLKGTFFVIRLVAGMGQNEPDGQGRVITINTASVAEFEGYQQAAYSASKGIYGMTL 180
DB 121 NLKGTFFVIRLVAGMGQNEPDGQGRVITINTASVAEFEGYQQAAYSASKGIYGMTL 180
QY 181 PIADLAPIGIRVMTIAGLFTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHLYQAI 240
DB 181 PIADLAPIGIRVMTIAGLFTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIRLDGAIKMP 261
DB 241 IENPFLNGEVIRLDGAIKMP 261

```

```

RESULT 3
Q9CTY3 PRELIMINARY; PRT; 261 AA.
AC 09CTY3:
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Hydroxyacyl-coenzyme A dehydrogenase, type II.
GN HSD17B10 OR HADH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

```

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., But C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Norioka P., Ring B., Schoenbach M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 CC EMBL: AK013340; BAB28800.1; -
 DR HSSP: O70351; IEGW.
 DR MGD: MGI:133871; Hsdl7b10.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 KW Oxidoreductase.
 SQ SEQUENCE 261 AA; 27273 MW; F36CD19C7FCEFAF CRC64;

Query Match 88.8%; Score 1158; DB 11; Length 261;
 Best Local Similarity 87.7%; Pred. No. 2, 2e-72;
 Matches 229; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 MAAYSVKGIYAVITGASGLIATRELVVGGASAVLDDPNSGGEAOAKLGNVCVF 60
 DB 1 MAAYSVKGIYAVITGASGLIATRELVVGGASAVLDDPNSGGEAOAKLGNVCVF 60
 DB 1 MAAYSVKGIYAVITGASGLIATRELVVGGASAVLDDPNSGGEAOAKLGNVCVF 60
 QY 61 APADYTSKDVOTATLALAKGKRGVAVVAVNCAGIAVASKTYNKKQGTHTLEDFORVLDV 120
 DB 61 APADYTSKDVOTATLALAKGKRGVAVVAVNCAGIAVASKTYNKKQGTHTLEDFORVLDV 120
 DB 61 APADYTSKDVOTATLALAKGKRGVAVVAVNCAGIAVASKTYNKKQGTHTLEDFORVLDV 120
 QY 121 NLMGTNVRILVAGEGQNEPDGQGRVITNTASVAAPEGGVQAASASGIVGMLT 180
 DB 121 NLMGTNVRILVAGEGQNEPDGQGRVITNTASVAAPEGGVQAASASGIVGMLT 180
 DB 121 NLMGTNVRILVAGEGQNEPDGQGRVITNTASVAAPEGGVQAASASGIVGMLT 180
 QY 181 PIARDAPIGIRVWTIAPGLFPTLTSLPEKYCNFLASQVPPSRLLGDPAYAHLYQAI 240
 DB 181 PIARDAPIGIRVWTIAPGLFPTLTSLPEKYCNFLASQVPPSRLLGDPAYAHLYQAI 240
 DB 181 PIARDAPIGIRVWTIAPGLFPTLTSLPEKYCNFLASQVPPSRLLGDPAYAHLYQAI 240
 QY 241 IENPFLNGEYIRLDGAIKROP 261
 DB 241 IENPFLNGEYIRLDGAIKROP 261
 DB 241 IENPFLNGEYIRLDGAIKROP 261

RESULT 4
 O8RTCV9 PRELIMINARY; PRT; 196 AA.
 AC O8RTCV9;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DE Endoplasmic reticulum-associated amyloid beta peptide-binding protein
 (fragment).
 GN ERAB.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Deininger M.H., Meyermann R., Schluesener H.J.;
 RT "Expression, release and induction of endoplasmic reticulum-associated
 amyloid beta-binding protein in brain disease.",
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY092415; BAB18189.1; -
 FT NON_TER 1
 FT NON_TER 196
 SQ SEQUENCE 196 AA; 20581 MW; 2400DE14966BAA6A CRC64;
 Query Match 76.2%; Score 993; DB 4; Length 196;
 Best Local Similarity 100.0%; Pred. No. 3, 8e-61;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 51 AKKLGNCVAPADYTSKDVOTATLALAKGKRGVAVVAVNCAGIAVASKTYNKKQGTHT 110
 DB 1 AKKLGNCVAPADYTSKDVOTATLALAKGKRGVAVVAVNCAGIAVASKTYNKKQGTHT 110
 DB 1 AKKLGNCVAPADYTSKDVOTATLALAKGKRGVAVVAVNCAGIAVASKTYNKKQGTHT 110
 QY 111 LEDFQRLDVNLMGTNVRILVAGEGQNEPDGQGRVITNTASVAAPEGGVQAASAS 170
 DB 111 LEDFQRLDVNLMGTNVRILVAGEGQNEPDGQGRVITNTASVAAPEGGVQAASAS 170
 DB 111 LEDFQRLDVNLMGTNVRILVAGEGQNEPDGQGRVITNTASVAAPEGGVQAASAS 170
 QY 171 SKGIVGMLTPIARDAPIGIRVWTIAPGLFPTLTSLPEKYCNFLASQVPPSRLLGDP 230
 DB 171 SKGIVGMLTPIARDAPIGIRVWTIAPGLFPTLTSLPEKYCNFLASQVPPSRLLGDP 230
 DB 171 SKGIVGMLTPIARDAPIGIRVWTIAPGLFPTLTSLPEKYCNFLASQVPPSRLLGDP 230
 QY 231 AEYAHLYQAIENPFL 246
 DB 231 AEYAHLYQAIENPFL 246
 DB 181 AEYAHLYQAIENPFL 196

RESULT 5
 Q19102 PRELIMINARY; PRT; 258 AA.
 ID Q19102;
 AC Q19102;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Probable 3-hydroxyacyl-CoA dehydrogenase F01G4.2 type II (EC 1.1.1.35)
 DE (Type II HADH).
 GN F01G4.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditiida;
 OC Rhabditiida; Peloderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Harris B.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA +
 NADH.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 FAMILY (SDR).
 CC EMBL: Z68341; CAA92764.1; -
 DR HSSP: O70351; IEGW.
 DR WormPep: F01G4.2; CE03127.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 KW Hypothetical protein; Oxidoreductase; NAD; Mitochondrion.
 FT NP_BIND 11 36 NAD (BY SIMILARITY).
 FT ACT_SITE 165 165 BY SIMILARITY.
 SQ SEQUENCE 258 AA; 27143 MW; 86BF2568E6902B3 CRC64;
 Query Match 57.5%; Score 750; DB 5; Length 258;
 Best Local Similarity 59.9%; Pred. No. 2, 9e-44;
 Matches 154; Conservative 35; Mismatches 66; Indels 2; Gaps 1;
 QY 3 AAAYSVKGIYAVITGASGLIATRELVVGGASAVLDDPNSGGEAOAKLGNVCVAP 62
 DB 3 AAAYSVKGIYAVITGASGLIATRELVVGGASAVLDDPNSGGEAOAKLGNVCVAP 62
 DB 2 SALRSTKGIYALVTGASGLGGAAYLAKAGQVAILDLPQSGADYAKKEIGG--ITP 59
 DB 2 SALRSTKGIYALVTGASGLGGAAYLAKAGQVAILDLPQSGADYAKKEIGG--ITP 59
 QY 63 ADYTSKDVOTATLALAKGKRGVAVVAVNCAGIAVASKTYNKKQGTHTLEDFORVLDVNL 122
 DB 63 ADYTSKDVOTATLALAKGKRGVAVVAVNCAGIAVASKTYNKKQGTHTLEDFORVLDVNL 122
 DB 60 ASVTSEEVRAAFVAVQAEYGRDALVACAGIAFAFKYSYQKKKHVDFAKIRQITIDVNV 119

NCBI_TaxID=305;
 [1]
 SEQUENCE FROM N.A.
 STRAIN-GM11000:
 MEDLINE-21681879; PubMed-11823852;
 RA Salanoubat M., Genin S., Attiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chander M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A., of the plant pathogen *Ralstonia solanacearum*.
 RT Genome sequence of the plant pathogen *Ralstonia solanacearum*.
 RL Nature 415:497-502(2002).
 DR EMBL; AL646070; CAD16241.1;
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR OXIDOREDUCTASE; Complete proteome.
 KW OXIDOREDUCTASE; Complete proteome.
 SQ SEQUENCE 252 AA; 25642 MW; D6EEFACDA99179DF CRC64;
 Query Match 52.9%; Score 689.5; DB 16; Length 252;
 Best Local Similarity 57.1%; Pred. No. 4,2e-40;
 Matches 145; Conservative 33; Mismatches 71; Indels 5; Gaps 3;
 QY 8 VAGLVAVITGASGSGILTAERLVGOGASAVLLDLPNSGGEAKKLGNCVFAPADYTS 67
 DB 3 INDQFVIVGASGSGAGATTALAGAGKVIADUNEAGALAOEIGR--FVACDVSS 60
 QY 68 EKDVOTATLAKGKRGVDVAVNCAGIAVASKTYNLRKGGTHLTEDFORVLDVNLGTFN 127
 DB 61 EADGGAAYOAT-SIGALAGLVNCAGIAPASRT--VCKAGPHLDQFARVININLIGTFN 117
 QY 128 VIRLVAGEGNEPPOGGRGVITNTASVAEFGOGVAASVSGKGVGMPTIARPLA 187
 DB 118 MRLATATATANAPNAGSERGVITNTASVAEFGOGVAASVSGVAMTLARPLA 177
 QY 188 PGIRVMTIAPGLFTPLTSLPEKVCNPLASQVFPSPRLGDPAEYAHVQAIIENPFLN 247
 DB 178 RGIRVMTIAPGLFTPLTSLPEKVCNPLASQVFPSPRLGDPAEYAHVQAIIENPFLN 237
 QY 248 GEYIRLDGAIKMP 261
 DB 238 GETIRLDGAIKMP 251
 RESULT 9
 006544 PRELIMINARY; PRT; 250 AA.
 AC 006544;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Oxidoreductase, short-chain dehydrogenase/reductase family.
 GN RY1144 OR MTC165.11 OR MTL117.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RC MEDLINE-98295987; PubMed-9634230;
 RA Cole S.T., Broesch R., Parthill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holtroyd S.,
 RA Hovnsy T., Jagsels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."

Nature 393:537-544(1998).
 [2]
 SEQUENCE FROM N.A.
 STRAIN-CDC 1551 / OSHKOSH;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Esmolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z95584; CAB09032.1;
 DR EMBL; AB006996; AAK45436.1;
 DR HSSP; O70351; 1E3S.
 DR TIGR; MTL177;
 DR TubercuList; RV1144;
 DR InterPro; IPR002198; ADH_short.
 DR InterPro; IPR00205; NAD_binding.
 DR Pfam; PF00106; adh_short; 1.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR Hypothetical protein; Complete proteome.
 KW SEQUENCE 250 AA; 25787 MW; 123A1005A12BD56 CRC64;
 Query Match 51.5%; Score 671.5; DB 16; Length 250;
 Best Local Similarity 60.1%; Pred. No. 7,2e-39;
 Matches 152; Conservative 25; Mismatches 69; Indels 7; Gaps 4;
 QY 9 KGVAVITGASGSGILTAERLVGOGASAVLLDLPNSGGEAKKLGNCVFAPADYTS 68
 DB 4 KDAVAVITGASGSGILTAERLVGOGASAVLLDLPNSGGEAKKLGNCVFAPADYTS 60
 QY 69 KDVOATATLAKGKRGVDVAVNCAGIAVASKTYNLRKGGTHLTEDFORVLDVNLGTFN 128
 DB 61 AAVSNALBELA-DSGPAVAVVNCAGTGNATRV--LSRDGVFPLAFAKKIYDINLVGTFN 117
 QY 129 IRLVAGEGNEPPOGGRGVITNTASVAEFGOGVAASVSGKGVGMPTIARPLA 188
 DB 118 LRLAERIAKTEP-IGERGVIINTASVAEFGOGVAASVSGKGVGMPTIARPLA 176
 QY 189 IGIRVMTIAPGLFTPLTSLPEKVCNPLASQVFPSPRLGDPAEYAHVQAIIENPFLN 248
 DB 177 KLIRVMTIAPGLFTPLTSLPEKVCNPLASQVFPSPRLGDPAEYAHVQAIIENPFLN 236
 QY 249 EYIRLDGAIKMP 261
 DB 237 EYIRLDGAIKMP 249
 RESULT 10
 092XSI PRELIMINARY; PRT; 255 AA.
 AC 092XSI;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Probable.
 GN RA0792 OR SMA1452.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Plasmid pSymA (megaplasmid 1).
 OC Bacteria; Proteobacteria; alpha subphylum; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1021;
 RC MEDLINE-21396509; PubMed-11481432;
 RA Barnett M.D., Fisher R.F., Jones I., Komp C., Abola A.P.,
 RA Bariloy-Hubler F., Bowser L., Capela D., Gallibert F., Gouzy J.,
 RA Gurjal M., Hong A., Hutzar L., Hyman R.W., Kahn D., Kahn M.D.,
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire

Thu Jun 26 06:55:09 2003

us-09-931-186-4.rspt

Page 7

```
DB 187 MTIAPGIFEPDMAGNTEEVNASTAGVPPPPRLGRPOEYAAALARIHTEENSMNGEVI RL 246
QY 254 DGAIRM 259
DB 247 DGAIRM 252

RESULT 13
Q8UF12 PRELIMINARY; PRT; 257 AA.
AC Q8UF12:
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE 3-hydroxyacyl-CoA dehydrogenase type II.
GN Atv1415 OR AGR_C_2613.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eissen J.A., Karp P.D., Boye D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Sempimachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Iano L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "the genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Hourlijo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Millin L.,
RA Houtmel K., Gordon J., Vaudin M., Iarchouk O., Epp A., Liu F.,
RA Flanagan C., Crowell C., Gunson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
DR EMBL: AE009102; AAL42421.1; -
DR EMBL: AE008067; AAK87207.1; -
KW Complete proteome.
SQ SEQUENCE 257 AA; 26622 MW; FF74A61FC4B2B5C CRC64;
```

```
QY 243 NPFLNGEVI RL DGAIRMOP 261
DB 238 NDYMNGEVIR L DGAIRMOP 256

RESULT 14
Q9DCX5 PRELIMINARY; PRT; 126 AA.
AC Q9DCX5:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE Hydroxyacyl-coenzyme A dehydrogenase, type II.
GN HSD17B10 OR HADH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=C5781/6J; TRISUP=KIDNEY;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Koehliwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staib F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima T., Mazzarelli J., Monbaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Williams L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:665-690(2001).
RN [1]
RP STIMULATORY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC CC
CC (SDR) FAMILY: BAB22046.1; -
DR EMBL: AK002368; BAB22046.1; -
DR HSSP: O70351; 1B6W.
DR MGD: MGI:1333871; Hsd17b10.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 126 AA; 13265 MW; 78FFB6D41B9989D CRC64;
```

```
Query Match 46.5%; Score 607; DB 11; Length 126;
Best Local Similarity 95.2%; Pred. No. 9e-35;
Matches 120; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```

ID      08R217;          PRELIMINARY;          PRT:      264 AA.
AC
DT      01-JUN-2002 (TREMBLrel. 21, Created)
DT      01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      3-hydroxyacyl-CoA dehydrogenase type II.
OS      Dictyostelium discoideum (Slime mold).
OC      Eukaryota; Eucetozoa; Dictyostelida; Dictyostelium.
OX      NCBI_TaxID=44689;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=AX4;
RA      Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA      Lehmann R., Baumgart C., Parra G., April J.F., Gulgo R., Kumpf K.,
RA      Tugend B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT      "Sequence and Analysis of Chromosome 2 of Dictyostelium.";
RL      Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR      EMBL; AC115594; RA192306.1;
SQ      SEQUENCE 264 AA; 28795 MW; 3C0007DA1309F294 CRC64;

```

erry Match	46.38;	Score 603.5;	DB 5;	Length 264;
st Local Similarity	48.88;	Pred. No. 3.7e-34;		
atches 127;	Conservative 46;	Mismatches 78;	Indels 9;	Gaps 5

```

OY      8 VKGVAVITVAGSAGLTGLAFAERLVQOGASAVYLLDLPNBSGSEBAQAKIGNN-CYFAAPADVT 66
Db      3 INGTFFVITVAGSAGLTLETSRRLRSIGANIFIMDMENBENGKRYVEELGSDKRTMESDYIT 62
OY      67 SEKDYCAALALAGKRGVDVAVNAGALAVASKTYNKKGGQTHTLEDFORULOVNIMNGTE 126
Db      63 LEDSVKSLSTEHCKAKRKEIHGVINCAGVAAARVVK-RDQVHPLDLEFTRVWVNNLIGTE 121
OY      127 NVYRIVAGEM-GONGED--QG-----GGVITINTASVAEFEGVOGAAVYASASGGVATGM 179
Db      122 NVYRLVADITHNONOSSKSDGDEEBEERKGVYIMTASVAEFEGVOGAAVYASASKSGVATGM 181
OY      180 LPIARDIAPICITVMTIAPGLGTPLITSLEPKVCNFIASVOAPPFRSLRQDAEYAHLYOA 239
Db      182 LPMARERATATKIKINTIAPGTETETPVEKMLPOLAIKSTINESIPPSRMRKKEPAFLCOH 241
OY      240 TIENPFLNGEIVRLDGAIRM 259
Db      242 TIENYINGEIVRLDGAIRL 261

```

RESULT 16
Q9ABU6
ID Q9ABU6 PRELIMINARY; PRT; 260 AA

DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-Mar-2002 (TREMBlrel. 20, last annotation update)
DE 3-hydroxyacyl-CoA dehydrogenase.
GN CC0124.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OC NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=211173698; Pubmed=11259647;
RA Nierman W.C., Feldlyum T.V., Laub M.R., Ohta N., Maddock J.R.,
RA Eisen J., Heidelberg J.F., Alley M.R., Chua N.,
RA Ptoczka J., Nelson W.C., Newton A., Stephens C., Phade N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolony J.F., Salt J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Ueberack T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of *Caulobacter crescentus*."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.

```

DR EMBL: AE005687, AAK2211.1; -.
DR HSP: 070351; 1E3S.
DR TIGR: CC0124; -.
DR InterPro: IPR002198; ADH_short.
DR InterPro: IPR00205; NAD_binding.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRPFAM1.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 260 AA; 27075 MW; 7DC145D069C89029 CRC64;
Query Match 45.6%; Score 595; DB 16; Length 260;
Best Local Similarity 51.0%; Pred. NO. 1.4e-33;
Matches 130; Conservative 30; Mismatches 89; Indels 6; Gaps 2

```

```
QY      11 LVAVITGSGSLGLATAERLVGGGASAVLLDPLPSGGGEQAOKKLGNCCYFAPADYTSK 70
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      7 VAAVVTGSGSLGEATARALAAQGVKVALEDMNERGLQVAKELGG -VFCKVNTSDAD 64
```

```

OY 7_ VQALALAGKFGGRDVAVNVCAGIVAKTYNLKKQTH-----LEFGCVLIVLMGFE 126
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 65 VDAGEFKAPAAAGQERILYNVCAGIGNAKTISRDKATGFKHPPLDAFRIIIOINLYGFE 124
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 127 NTVRLVAGEMGONEPDGGGRGVIIINTASVAAEFGQVGOAAYSASKSGIVGMLPIARDL 186
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 125 RCLAKSARKMDLEPLEDGERGAIINTASVAAEFGQVGOAAYSASKSGVVGMLPIARDL 184
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 187 APLGIRVMTIAPGLGTPPLTSLSPKVCNFTLASOVPPPSRLGDPATYAHLYOAIINPPL 246
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 185 MGEIGIVNTIILGIFNTPLMNNAPPAVAKVAGLAASVPPPKRLGHEEYEAQALATIMIGYF 244
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 247 NGEVIRLDGAINMP 261
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 245 NGEDVRLDGINMAP 259
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 17
Q93SU3
ID Q93SU3 PRELIMINARY; PRT; 443 AA

DT 01-DEC-2001 (TIMBrel, 19, Created)
DT 01-DEC-2001 (TIMBrel, 19, last sequence update)
DT 01-JUN-2002 (TIMBrel, 21, last annotation update)
DE ucsc-3p.
OS *Myxococcus xanthus*.
OC Bacteria; Proteobacteria; delta subdivision; Myxobacteriia
OC Myxococcales; Cytyobacterineae; Myxococcaceae; Myxococcus
OC NCBI_taxid=34;

RC STRAIN=CECT 422;
RA Poza M., Sielro C., Villa T.G.;
RT "Clone USC5 from *Myxococcus xanthus* CECT 422 strain.";

```
CC      -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CD      (SDR) FAMILY.
CC      EMBL: AY034405; AKK49009.1; -.
DR      InterPro: IPR002198; ADH_short.
DR      InterPro: IPR001059; EF-P.
DR      InterPro: IPR001092; HTH_basic.
DR      Pfam: PF00106; adh_short.1.
DR      Pfam: PF01132; EFp-1.
DR      PROSITE: PS00061; ADH_SHORT_UNKNOWN_1.
DR      PROSITE: PS00038; HELIX_LOOP_HELIcity_UNKNOWN_1.
KM      Oxidoreductase.
SQ      SEQUENCE   443 AA;  47589 MW;  21157E0FD55FA20 CRC64;

Query Match          29.6%; Score 386; DB 2; Length 443;
Best Local Similarity 46.4%; Pred. No. 6,7e-18;
Matches    96; Conservative    29; Mismatches    70; Idels    12; Gaps    5

QY      13 AVITG---GASGLGIATAE-RLVGGAGSAVLLDLPNSGGEAQAOKKIG-NNCVFAPADVT 66
||||| : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```



```

Db      8 AVITGWMXXRXBAGRPAPRRRL-----ARSALFLDNDKCAAAVAGLCAKARAFYNNVS 63
QY      67 SEKDQVOTLALAKGKFGVDVAVNAGIAVASKTYNKKGGTHLEDFORLVDNMGTF 126
Db      64 DEAAVTAIDQAHDFLGGGLNVAMNAGILGAGRV--LCKEGPMPLAGFGQTVNVLGSE 121
QY      127 NVIRLVAGEMGONEDDGGORGVIINTASVAAFEGOVQAAVSASKGGIVGMLPIARDL 186
Db      122 NVAKAAARMQHNENAGTGERGVIIINTASIAAYEGQIAAAYASKGGVSMILPMAREL 181
QY      187 APGIRVMTIAPGLGFTPLTSLPEKV 213
Db      182 SREGRVNTIAPGVWTPWDMGMPRAV 208

RESULT 18
08XHL1
ID      08XHL1      PRELIMINARY:      PRT:      246 AA.
AC      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2002 (TREMBlrel. 20, last sequence update)
DE      01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE      3-oxoacyl-[acyl-carrier-protein] reductase.
GN      FABG OR CPE1070.
OS      Clostridium perfringens.
OC      Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC      Clostridiales; Clostridiaceae; Clostridium.
OX      NCBI_TaxID=1502;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=13 / TYPE A;
RX      PubMed=11792842;
RA      Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA      Shiba T., Ogasawara N., Hattori K., Kohara S., Hayashi H.;
RT      Complete genome sequence of Clostridium perfringens, an anaerobic
RT      flesh-eater."
RL      EMBL: AF003189; BAB80776.1; -
DR      InterPro: IPR002198; ADH_short.
DR      Pfam: PF00106; adh_short.1.
DR      PRINTS: PR00080; SDRFAMILY.
DR      PROSITE: PS00061; ADH_SHORT; 1.
KW      Complete proteome.
SQ      SEQUENCE 246 AA; 26267 MW; CD90B8C650ECC817 CRC64;

Query Match      28.6%; Score 373.5; DB 16; Length 246;
Best Local Similarity 35.8%; Pred. No. 2.4e-18;
Matches 93; Conservative 47; Mismatches 97; Indels 23; Gaps 7;

```

```

AC      099YD6;
DT      01-JUN-2001 (TREMBlrel. 17, Created)
DT      01-JUN-2001 (TREMBlrel. 17, last sequence update)
DE      01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE      Putative beta-ketoacyl-ACP reductase (EC 1.1.1.100).
GN      FABG OR SPY1749.
OS      Streptococcus pyogenes.
OC      Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC      Streptococcaceae; Streptococcus.
OX      NCBI_TaxID=1314;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
RX      MEDLINE=21192684; PubMed=11296296;
RA      Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA      Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lal H.S., Lin S.P.,
RA      Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA      Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT      Complete genome sequence of an M1 strain of Streptococcus pyogenes."
RL      Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001)
CC      -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC      (SDR) FAMILY.
DR      EMBL: AE006603; AAK34493.1; -
DR      HSSP: P50162; IAE1.
DR      InterPro: IPR002198; ADH_short.
DR      InterPro: IPR001092; H1H_basic.
DR      Pfam: PF00106; adh_short; 1.
DR      PRINTS: PR01608; BACTINVASINC.
DR      PRINTS: PR00080; SDRFAMILY.
DR      PROSITE: PS00061; ADH_SHORT; 1.
DR      PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW      Oxidoreductase; Complete proteome.
SQ      SEQUENCE 244 AA; 26002 MW; 67EC23870D40D65 CRC64;

Query Match      27.3%; Score 355.5; DB 16; Length 244;
Best Local Similarity 35.4%; Pred. No. 4.2e-17;
Matches 92; Conservative 41; Mismatches 102; Indels 25; Gaps 5;

```

RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 15692 / PAOI;
 RX MEDLINE-2043737; PubMed-10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltz L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardis K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reiter J., Satter M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT Complete genome sequence of *Pseudomonas aeruginosa* PAOI, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDS) FAMILY.
 DR EMBL: AE004854; AAG07777.1; -.
 DR HSSP: P50163; 2AE1.
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR001064; Crystal11n.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 DR Oxidoreductase; Complete proteome
 KW SEQUENCE 252 AA; 26720 MW; F1F445AB82C2D8DE CRC64;
 QY Query Match 27.2%; Score 355; DB 16; Length 252;
 Best Local Similarity 35.1%; Pred. No. 4.7e-17;
 Matches 94; Conservative 40; Mismatches 100; Indels 34; Gaps 7;
 Db 3 LKDKVILITGGCGGLRANGELAGKALVLDLNRERLDVAVACRAAGDARA----- 58
 QY 8 VKGLVAVITGASGLATAEERLVGGASAVLLDPN-----SGGEAQAKKLG 55
 Db 59 -YCVNVADEQYTHVAVAGVADFGALINGVANNAGILRGLITKVDQLSKKSLAQ 113
 QY 56 NNCVFAADVTSKEDVOTALALAKGKGRVDVAVNCAGIYAVASKYNNKKGQTH--TLED 113
 Db 114 FORVLVNLMTGNTNRLVAGMGQ--NEPDGOGRGVITNMAVAAFEQVGOAAYAS 171
 QY 114 MOSVIDVNLTVGLCTREVAAKKTELKNE-----GALVNTSSISR-AGNGOANYSA 165
 Db 172 KGSIVMTPIADLPIGIRWTIAPGLFGLPLTSLPEKYCNFLASQVPPSRUGDPA 231
 QY 166 KAGVADTVYMAKELARGIRAVGAPFLETETEMTAGMKPEALKEKTAGIPL-KRMGRV 224
 Db 232 EYAHLYQAITENPFLNGEVIRLDGAR 259
 QY 225 EIAHSAVYIRENDYVYGRVLELDGRL 252
 Db
 RESULT 21
 Q97DA6 PRELIMINARY; PRT; 249 AA.
 AC 097DA6;
 DT 01-OCT-2001 (TREMblrel. 18, Created)
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE 3-ketocacyl-acyl carrier protein reductase.
 GN CAC3574.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE-21359325; PubMed-11466286;
 RA Neelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gidson R., Lee H.W., Dubois J., Qiu D., Hilti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucelte-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.,
 RT genome sequence and comparative analysis of the solvent-producing
 RT bacterium *Clostridium acetobutylicum*.";
 RL J. Bacteriol. 183:4823-4838(2001).

DR EMBL: AE007854; AAK81497.1; -.
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 KW Complete proteome.
 QY SEQUENCE 249 AA; 26247 MW; B13D7EAC21A626A CRC64;
 QY Query Match 26.3%; Score 343.5; DB 16; Length 249;
 Best Local Similarity 33.2%; Pred. No. 2.9e-16;
 Matches 86; Conservative 56; Mismatches 96; Indels 21; Gaps 6;
 Db 8 VKGLVAVITGASGLATAEERLVGGASAVLLDPN-----AKKIGNNVFAP 62
 Db 5 LSGVAVAVTGGAGRLGALIKLAEGANLV-VNYSSEAEYOKLKEIEELSKAVAYK 63
 QY 63 ADVTSKEDVOTALALAKGKGRVDVAVNCAGIYAVASKYNNKKGQTHLEDQFQVLDVNL 122
 Db 64 ADISKYDEAEITIKKALDEYGVLDLVNNAITGKDLLRMKE-----EDFQSVINVL 117
 QY 123 MGTNVRILVAGMGQNEPDGOGRGVITNMAVAAFEQVGOAAYASAGSGVIGMTLP 182
 Db 118 KGANCKIKHYSRVMLK-----KSGKITINSSVIGLIGNAGOVNIAAKAGIIGTKSV 171
 QY 183 ARDLAPIGIRWTIAPGLFGLPLTSLPEKYCNFLASQVPPSRUGDPAEYAHLYQAIIE 242
 Db 172 AKELASRGITVNAVAPGILKSDMTDALDKORRESIYAVPL-NVGEAEADVNLVFLAS 230
 QY 243 --NPLNGEVIRLDGAR 259
 Db 231 DLSSTTGQVIVDVGMY 249
 Db
 RESULT 22
 Q9R9W0 PRELIMINARY; PRT; 247 AA.
 AC 09R9W0;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Dehydrogenases with different specificities (related to short-chain
 DE alcohol dehydrogenases).
 GN PABG3 OR TRE1472
 OS Thermoaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Thermoaerobacteriales; Thermoaerobacteriaceae; Thermoaerobacter.
 OX NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MBAT / JCM11007;
 RX MEDLINE-21992816; PubMed-11997336;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.,
 RT "A complete sequence of *T. tengcongensis* genome.";
 RT Genome Res. 12:689-700(2002).
 DR EMBL: AE013105; AAM24694.1; -.
 KW Complete proteome.
 QY SEQUENCE 247 AA; 26606 MW; 357D82B8C60E7947 CRC64;
 QY Query Match 25.9%; Score 337.5; DB 16; Length 247;
 Best Local Similarity 34.3%; Pred. No. 7.4e-16;
 Matches 87; Conservative 48; Mismatches 100; Indels 19; Gaps 6;
 Db 12 VAVITGASGLATAEERLVGGASAVLLDPN-----QAKKIGNNVFAPADYTS 67
 Db 7 VAFVVGSGRGIGRALAVLADGEFIATYVKDKSABEVEEKKHGVDLAKCDVSK 66
 QY 68 EKDVOITALAKKGRGRVDVAVNCAGIYAVASKYNNKKGQTHLEDQFQVLDVNLMTFN 127
 Db 67 YHEVKAIVEKYLEEGSIDVYVNNAGITKDLILKME-----EMDQVIVDVLKGAFN 120

```

QY 128 VRLVAGENGQNEPDGQGVINTASVAEFGVGAAYASAKGIVGMLPIARDIA 187
DB 121 VIKFASKYMIKK-----RKGINISSYVGLMGNQANYAASKRGIIGLTRKSAKELA 174
QY 188 PIGIRMTIAPGIFGPELLTSLPEKVCNPLASQVPPSRIGDPAEFAHLVQ--AIENPF 245
DB 175 SRGITYNAVAPGFIETDMTNLTKEDIKEMLKSIPL-KRAGNPEEVAEVAFLASSADY 233

QY 246 LNGEVIRLDGAIRM 259
DB 234 ITGOVINVDGWMV 247

RESULT 23
Q42774 PRELIMINARY; PRT; 297 AA.
ID 042774;
AC 042774;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE 3-oxoacyl-(acyl-carrier-protein)-reductase.
GN OAR-1 OR BZA19.180.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
ON NCBI_TaxID=5141.
RX [1]
RP SEQUENCE FROM N.A.
RA Burger F., Bros B., Weiss H.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte U., Altm V., Hohelsel J., Brandt P., Fatmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhapt G.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
CC (SDR) FAMILY.
DR EMBL; AF042860; AAB99799.1; -.
DR EMBL; AF042860; CAB98248.1; -.
DR HSSP; O70351; IB6W.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short.1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT.1.
KW Oxidoreductase.
SQ SEQUENCE 297 AA; 31342 MW; 8DC08FEDF584196F CRC64;

Query Match 25.8%; Score 336.5; DB 3; Length 297;
Best Local Similarity 31.6%; Pred. No. 1.1e-15;
Matches 97; Conservative 40; Mismatches 103; Indels 67; Gaps 8;

QY 5 VRSGKGLVAVITGASGLATAERLYVGASAVLLDLPNS-----GGGA 49
DB 1 MRSILHQAALITGGSSIGLAIARLYLBECSTVLGRTSTIGRASQSLLSQPLHSPA 60
QY 50 QAKKIGNNCFAPADVTSEKDVOTAL-ALAKGFRVDVAVNAGIAVAS--KTYNKK 105
DB 61 QQPSDTRKVSYHPLNVAASSWEDLQSNKSGKGRVDILINCAGITORSPLMKT----- 115
QY 106 GQHTLEDQRYVDVNMGTENVIRLYAGEMQNEP-----DQGG----- 145
DB 116 -----SIEVEGLDITNLRGTVLGCKFGRALNRREBQCHPRYKADGGAGEGVMEGTTEE 171
QY 146 -----QGVIIINTASVAEFGVGAAYASAKGIVGMLPIARDIAPIG 190
DB 172 GKSGKQGVREGVQENGVIIINVASILAKQVIGTSTVYAAKAGVGLTSLAHEGRSG 231
QY 191 IRVMTIAPGLFGPIPLTSLPEKVCNPLASQVPPSRIGDPAEFAHLVQAIENPFLNGEV 250

```

```

DB 232 IRVNAVLPGFIETDMTNLKNP-----SILQIPL-GRGCTQDEVADALFLIKNRYANNCV 287
QY 251 IRLDGAIR 257
DB 288 IRLDGL 294

RESULT 24
Q9KA03 PRELIMINARY; PRT; 246 AA.
ID Q9KA03;
AC Q9KA03;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE 3-oxoacyl-(acyl-carrier-protein) reductase (EC 1.1.1.100).
GN FABG OR BH2451.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacilliales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Masui N.,
RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
CC (SDR) FAMILY.
DR EMBL; AP001515; BAB06210.1; -.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short.1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 246 AA; 26126 MW; 852B95EBDBE9E90 CRC64;

Query Match 25.6%; Score 333.5; DB 16; Length 246;
Best Local Similarity 34.2%; Pred. No. 1.4e-15;
Matches 90; Conservative 42; Mismatches 102; Indels 29; Gaps 7;

QY 8 VRGLVAVITGASGLATAERLYVGASAVLLDLPNSGGE-----AQAKKIGNNCF 59
DB 2 LOGKTAIVTGAISRGIGRATAMELARHGAVVV---NYAGNKEKAEKVVAEIKELGVPAI 57
QY 60 PAPADVTSEKDVOTALAKAGFRVDVAVNAGIAVASKTYNKKGQHTLEDQRYVD 119
DB 58 AIGADVADSESVQAMVKETIDIFGAVDILVNNAGITRDLEFKME-----EDWDVID 111
QY 120 VMLGTFENIRLYVAGEMQNEPDQGOR-GVLIINTASVAEFGVGAAYASAKGIVGM 178
DB 112 TULKGVFHCASKAVTSPMK-----QGRGRIINSSYVGAIGNQANYAAKAGVIGL 164
QY 179 TLPPIARDIAPIGIRVMTIAPGLFGPIPLTSLPEKVCNPLASQVPPSRIGDPAEFAHLVQ 238
DB 165 TLTIAELANRNITVNAVAPGFIETDMGTGELPEDEVAKMLGOIPL-ARLGOPEEVAKAVR 223
QY 239 AIEN--PFLNGEVIRLDGAIRM 259
DB 224 FLASDDASLYLTGQTIHVNGWMV 246

RESULT 25
Q8YVTO PRELIMINARY; PRT; 251 AA.
ID Q8YVTO;
AC Q8YVTO;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

```

DE 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase.
GN FABG OR ALR1894.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; Pubmed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Matanabe A., Iriuguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
RL EMBL, AF003587; BAB73593.1; -;
DR InterPro: IPR002198; ADH_short.
DR InterPro: IPR001092; HLH_basic.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRfamily.
DR PROSITE: PS00061; ADH_SHORT; 1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KM Complete proteome.
SQ SEQUENCE 251 AA; 26218 MW; 57D0712F8E6B698 CRC64;

Query Match 25.6%; Score 333.5; DB 16; Length 251;
Best local similarity 33.1%; Pred. No. 1.4e-15;
Matches 91; Conservative 46; Mismatches 97; Indels 41; Gaps 7;

QY 1 MAAAVRSYKGLVAVITGASGLATAERIVGOGASA-----VLLDLPNSGG 47
DB 1 MALTISENLRGQVAVVVGASRGIGRAITALELANTGATVVVNVASSSTADEVVAETGAGG 60
QY 48 EAQAKKLGNNCVAFADVTSEKDVQATALAKGKFGRVDAVAVACAGIAVAASKTYNLKQG 107
DB 61 EAVALK-----ADVSGVEQVDNLNGAIDKFKRIDILVNNAGITRDITLLRMKP-- 109
QY 108 THHIEDFQRYLDVNMKGTENVIRLVAGEKGNEDDGGRGVITINTASVAAPFGVGOAA 167
DB 110 ---EDQAVIDINLGLVFLCTRAVSKMLKQ-----RSGRIINITSVAGQGNPQAN 159
QY 168 YSASKGIVGMLPIADLAPIGIRVWTIAPGLFGTPLTSLPEKYCNFLASQVPPPSRL 227
DB 160 YSAKAGVIGFTVAKELASRGITVAVAAPGFATDMTSNLKSE---GILQYIPL-GRY 215
QY 228 GDPREYAHLYQALLENP---FLNGEVYRLDGAIRM 259
DB 216 GQPEIAGWVRFLLADPAAPAAVITGQVFNVDDGVM 250

Search completed: June 23, 2003, 14:32:44
Job time : 33.6667 secs

Thu Jun 26 06:55:08 2003

us-09-931-186-4.rsp

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 14:19:47 ; Search time 7.83333 Seconds

(without alignments)
1381.956 Million cell updates/sec

Title: US-09-931-186-4

Perfect score: 1304
Sequence: 1 MAAVRKVKGLAVITGGAS.....ENPFLNGEYTRLDGAIKMP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1299	99.6	261	1	HCD2_HUMAN
2	1196	91.7	261	1	HCD2_BOVIN
3	1166	88.7	260	1	HCD2_RAT
4	1137	87.2	261	1	HCD2_MOUSE
5	908	69.6	255	1	HCD2_DROME
6	383.5	29.4	247	1	YD50_MYCTU
7	341	26.2	246	1	FABG_THEMA
8	334	25.6	261	1	DHB8_HUMAN
9	334	25.6	320	1	FABG_CUPLA
10	328.5	25.2	244	1	FABG_VIBCH
11	315.5	24.2	260	1	DHB8_MOUSE
12	313.5	24.0	247	1	FAG1_SYNY3
13	309.5	23.7	246	1	FABG_BACSU
14	305	23.4	260	1	YK02_MYCTU
15	301	23.1	255	1	YWFD_BACSU
16	300	23.0	255	1	1BHD_STRPX
17	294.5	22.6	548	1	Y4V1_RHISM
18	293	22.4	249	1	BAV1_EUBSP
19	291.5	22.4	244	1	FABG_VIBHA
20	290.5	22.3	248	1	FABG_AQUAE
21	289.5	22.2	244	1	FABG_ECOLI
22	288	22.1	263	1	UCPA_SALTY
23	287.5	22.0	246	1	PHBB_ALCEU
24	286	21.9	248	1	PHAB_ACISS
25	284.5	21.8	256	1	Y019_THEMA
26	283.5	21.7	244	1	FABG_SALTY
27	281.5	21.6	249	1	NODG_AZOB
28	280	21.5	259	1	CTMB_PSEPU
29	279.5	21.4	241	1	PHBB_ZOORA
30	279.5	21.4	248	1	FABG_CHLMT
31	277.5	21.3	289	1	YHDF_BACSU
32	277	21.2	250	1	LINC_PSEPA
33	276	21.2	249	1	BAV2_EUBSP

34	276	21.2	263	1	UCPA_ECO57
35	276	21.2	263	1	UCPA_ECOLI
36	276	21.2	319	1	FABG_ARATH
37	275	21.1	246	1	PHBB_CHRVI
38	272	20.9	250	1	LINC_PSEPA
39	272	20.9	251	1	Y325_THEMA
40	270.5	20.7	240	1	FAG2_SYNY3
41	270.5	20.7	247	1	FABG_CHLTR
42	269.5	20.7	251	1	DHXR_STRCM
43	268.5	20.6	262	1	DHGB_BACME
44	267.5	20.5	336	1	TS2_MAIZE
45	266.5	20.4	241	1	PHBB_RHIME
46	266.5	20.4	242	1	FABG_HAEIN
47	264	20.2	247	1	FABG_MYCTU
48	261	20.0	261	1	DHGA_BACME
49	259	19.9	258	1	DHGB_BACSU
50	259	19.9	261	1	DHG3_BACME
51	259	19.9	261	1	DHG3_BACME
52	258.5	19.8	238	1	Y0XD_BACSU
53	258	19.8	251	1	DHG2_BACME
54	257	19.7	256	1	BUDC_KLEPN
55	257	19.7	261	1	DHG4_BACME
56	256	19.6	261	1	DHG1_BACME
57	254.5	19.5	261	1	FABG_RICPR
58	254	19.5	261	1	SORD_KLEPN
59	251.5	19.3	267	1	PGDH_HUMAN
60	250.5	19.2	266	1	YHXC_HUMAN
61	250.5	19.2	285	1	Y4MP_RHISM
62	250	19.2	285	1	Y4MP_RHISM
63	246.5	18.9	261	1	3BHD_COMTE
64	245.5	18.8	253	1	YV06_PSEAE
65	245	18.8	255	1	GNO_GLIOX
66	245	18.8	256	1	NODG_RHIS3
67	244.5	18.8	245	1	NODG_RHIS3
68	244.5	18.8	262	1	YXBG_BACSU
69	243	18.6	270	1	DHMA_FLAS1
70	241.5	18.5	258	1	BDHA_RHIME
71	239	18.3	255	1	BDHA_ECOLI
72	238	18.3	247	1	FABG_PSEAE
73	237.5	18.2	261	1	FAGCW_ECOLI
74	237	18.2	248	1	FABG_CHLPA
75	237	18.2	255	1	FABG_MYCAV
76	235	18.0	257	1	YXJF_BACSU
77	228.5	17.6	245	1	NODG_RHIME
78	227.5	17.4	894	1	FOX2_NEOCR
79	227.5	17.4	258	1	BDHA_ALCEU
80	226.5	17.4	242	1	PHAB_PARDE
81	226.5	17.4	273	1	TEN1_DANST
82	224.5	17.2	249	1	DEK2_STRYN
83	224.5	17.2	256	1	DHSG_RHOSH
84	224	17.2	254	1	TDNO_ECOLI
85	223.5	17.1	241	1	BUDC_KLETE
86	222.5	17.1	256	1	MTDH_URORA
87	222.5	17.1	900	1	FOX2_YEAST
88	221.5	17.0	285	1	GS39_BACSU
89	221	16.9	255	1	FABG_MYCSM
90	220.5	16.9	272	1	FABG_MYCAB
91	219.5	16.8	259	1	SRID_ECOLI
92	217	16.6	248	1	Y452_LISIN
93	217	16.6	254	1	KDUD_BACSU
94	216.5	16.6	253	1	KDUD_ECOLI
95	215	16.5	134	1	FABG_ACTGA
96	213	16.3	142	1	DHB8_CALTA
97	212.5	16.3	248	1	Y432_LISMO
98	212	16.3	281	1	BPHB_COMTE
99	212	16.3	281	1	YHXB_BACSU
100	211.5	16.2	278	1	Y4LA_RHISM

ALIGNMENTS

RESULT 1

HC02_HUMAN
 ID HC02_HUMAN STANDARD: PRT: 261 AA.
 AC Q99714;
 DT 01-NOV-1997 (rel. 35, Created)
 DT 01-NOV-1997 (rel. 35, Last sequence update)
 DE 15-JUN-2002 (rel. 41, Last annotation update)
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)
 DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein) (Short-chain type dehydrogenase/reductase XH98G2).
 GN HADH2 OR ERAB OR XH98G2 OR SCHAD.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=97478528; PubMed=9338779;
 RA Yan S.D., Fu J., Soto C., Chen X., Zhu H., Al-Mohanna F., Collinson K., Zhu A., Stern E., Saido T., Tomiyama M., Ogawa S., Rohrer A., Stern D.;
 RT "An intracellular protein that binds amyloid-beta peptide and mediates neurotoxicity in Alzheimer's disease."
 RL Nature 389:689-695(1997).
 [2]
 RP SEQUENCE FROM N.A.
 RA Zhuchenko O.P., Wehnert M., Bailey J., Sun Z.S., Lee C.C.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98337980; PubMed=9671743;
 RA Miller A.P., Willard H.F.;
 RT "Chromosomal basis of X chromosome inactivation: Identification of a multigene domain in Xp11.21-p11.22 that escapes X inactivation."
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8709-8714(1998).
 [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=98221216; PubMed=9553139;
 RA He X.Y., Schulz H., Yang S.Y.;
 RT "A human brain L-3-hydroxyacyl-coenzyme A dehydrogenase is identical to an amyloid beta-peptide-binding protein involved in Alzheimer's disease."
 RL J. Biol. Chem. 273:10741-10746(1998).
 [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Lung;
 RA Strausberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: BINDS INTRACELLULAR AMYLOID-BETA. BY INTERACTING WITH AMYLOID-BETA, IT MAY CONTRIBUTE TO THE NEURONAL DYSFUNCTION ASSOCIATED WITH ALZHEIMER DISEASE.
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN NORMAL TISSUES BUT IS OVEREXRESSED IN NEURONS AFFECTED IN AD.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U96132; AAC51812.1; -
 CC EMBL: U73514; AAB69858.1; -
 CC EMBL: AF06914; AAC39900.1; -
 CC EMBL: AF03555; AAC15902.1; -
 CC EMBL: AF037438; AAC16419.1; -
 CC -----

DR EMBL: BC000372; AAH00372.1; -
 DR HSSP: O70351; 1E3S.
 DR Genew: HGNC:4800; HADH2.
 DR MIM: 300256; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KM Oxidoreductase; NAD.
 FT NP_BIND 12 37 NAD (BY SIMILARITY).
 FT ACT_SITE 168 168 BY SIMILARITY.
 SQ SEQUENCE 261 AA; 26923 MW; 9E74F242E3BEFE1 CRC64;
 Query Match 99.6%; Score 1299; DB 1; Length 261;
 Best Local Similarity 99.6%; Pred. No. 8.4e-94;
 Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAAVRSYKGLVAVITGASGLGATFARLTVGOGASAVLDPNSGGEAQAQKLNCCYF 60
 DB 1 MAACRSYKGLVAVITGASGLGATFARLTVGOGASAVLDPNSGGEAQAQKLNCCYF 60
 QY 61 APADYTSKDVOTATLAKGKFGKRVDAVNCAGIAVASKTYNLRKQHTLLEDFORVLDV 120
 DB 61 APADYTSKDVOTATLAKGKFGKRVDAVNCAGIAVASKTYNLRKQHTLLEDFORVLDV 120
 QY 121 NMGTFENVIRLVAGEMGNEDDGGORGVIIINTASVAAFEGOVGAAYASAKSGIVGNTL 180
 DB 121 NMGTFENVIRLVAGEMGNEDDGGORGVIIINTASVAAFEGOVGAAYASAKSGIVGNTL 180
 QY 181 PIARDLPIGIRVMTIABGLFTPLTSLPEKVCNFIASQVPPSRIGDPAEYVHLVQAI 240
 DB 181 PIARDLPIGIRVMTIABGLFTPLTSLPEKVCNFIASQVPPSRIGDPAEYVHLVQAI 240
 QY 241 IENPFLNGEVTRLDGAIKMP 261
 DB 241 IENPFLNGEVTRLDGAIKMP 261
 RESULT 2
 ID HC02_BOVIN STANDARD: PRT: 261 AA.
 AC O02691;
 DT 15-JUL-1998 (rel. 36, Created)
 DT 15-JUL-1998 (rel. 36, Last sequence update)
 DE 16-OCT-2001 (rel. 40, Last annotation update)
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH).
 GN HADH2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE-Liver;
 RX MEDLINE=97214648; PubMed=9061028;
 RA Furuta S., Kobayashi A., Miyazawa S., Hashimoto T.;
 RT Cloning and expression of cDNA for a newly identified isozyme of bovine liver 3-hydroxyacyl-CoA dehydrogenase and its import into mitochondria.
 RL Biochim. Biophys. Acta 1350:317-324(1997).
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

entitles requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; AB002156; BAA19510.1; -
 DR HSSP; 070351; 1E6W;
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KM Oxidoreductase; NAD; Mitochondrion.
 FT NP_BIND 12 NAD (BY SIMILARITY).
 FT ACT_SITE 168 168 BY SIMILARITY.
 SQ SEQUENCE 261 AA: 27140 MW: 807572B6A9A9780 CRC64:

Query Match 91.7%; Score 1156; DB 1; Length 261;
 Best Local Similarity 91.6%; Pred. No. 8e-86;
 Matches 229; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MAARVSVKGLAVITGGASGLTAEIRIVGSGASAVLLDLPNSGGEAOKKIGNVFE 60
 DB 1 MAARVSVKGLAVITGGASGLTAEIRIVGSGASAVLLDLPNSDGETOAKKLGKSCAF 60
 QY 61 APADVTSEKDVOTALALAKGKFRVDVAVNCAGIAVASKTYNLKKGQTHLEDFQRVLDV 120
 DB 61 APADVTSEKDVOTALALAKGKFRVDVAVNCAGIAVASKTYNLKKGQTHLEDFQRVLDV 120
 QY 121 NMAGFNVIRLVAGMGONEPQGGQGVYINTASVAAPFEGVGGAAASASGKIVGNTL 180
 DB 121 NMAGFNVIRLVAGMGONEPQGGQGVYINTASVAAPFEGVGGAAASASGKIVGNTL 180
 QY 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFRLDPAEYAHVQAI 240
 DB 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFRLDPAEYAHVQAI 240
 QY 241 ENPFLNGEVIIRLDGAIKMP 261
 DB 241 ENPFLNGEVIIRLDGAIKMP 261

RESULT 3

HCD2_RAT STANDARD; PRT; 260 AA.

ID HCD2_RAT 070351; 09QYD.

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)

DE (Endoplasmic reticulum-associated amyloid beta-peptide binding

protein).

GN HADH2 OR ERAB.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_Taxid=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Gunn-Moore F.J.; Tavares J.M.;

RT "Rattus norvegicus amyloid beta-peptide binding protein (ERAB) mRNA.";

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

RT "Recognition of structurally diverse substrates by type II

RT 3-hydroxyacyl-CoA dehydrogenase (HADH II)/amyloid-beta binding

RT alcohol dehydrogenase (ABAD).";

RL J. Mol. Biol. 303:311-327(2000).

CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA

CC + NADH.

CC -1- SUBUNIT: HOMOTETRAMER.

CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

CC (SDR) FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

DR EMBL; AF049878; AAC05747.1; -

DR EMBL; AF069770; AAF14853.1; -

DR PDB; 1E3W; 25-MAY-01.

DR PDB; 1E3S; 25-MAY-01.

DR PDB; 1E6W; 25-MAY-01.

DR InterPro; IPR002198; ADH_short.

DR Pfam; PF00106; adh_short; 1.

DR PRINTS; PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH_SHORT; 1.

KM Oxidoreductase; NAD; Acetylation; 3D-structure.

FT INCT_MET 0

FT MOD_RES 1 ACETYLATION (BY SIMILARITY).

FT NP_BIND 11 NAD (BY SIMILARITY).

FT ACT_SITE 167 167 BY SIMILARITY.

FT CONFLICT 4 V -> C (IN REF. 2).

FT SEQUENCE 260 AA: 27114 MW: 3078723A95F9227 CRC64:

Query Match 88.7%; Score 1156; DB 1; Length 260;

Best Local Similarity 88.1%; Pred. No. 1e-82;

Matches 229; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 2 AAARVSVKGLAVITGGASGLTAEIRIVGSGASAVLLDLPNSGGEAOKKIGNVFA 61
 DB 1 AAARVSVKGLAVITGGASGLTAEIRIVGSGASAVLLDLPNSGEGTEAKKLGKSCAF 60
 QY 62 PADVTSEKDVOTALALAKGKFRVDVAVNCAGIAVASKTYNLKKGQTHLEDFQRVLDV 121
 DB 62 PADVTSEKDVOTALALAKGKFRVDVAVNCAGIAVASKTYNLKKGQTHLEDFQRVLDV 120
 QY 122 LMGTENVIRLVAGMGONEPQGGQGVYINTASVAAPFEGVGGAAASASGKIVGNTL 181
 DB 122 LMGTENVIRLVAGMGONEPQGGQGVYINTASVAAPFEGVGGAAASASGKIVGNTL 180
 QY 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFRLDPAEYAHVQAI 241
 DB 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFRLDPAEYAHVQAI 240
 QY 241 ENPFLNGEVIIRLDGAIKMP 261
 DB 241 ENPFLNGEVIIRLDGAIKMP 260

RESULT 4

HCD2_MOUSE STANDARD; PRT; 261 AA.

ID HCD2_MOUSE 008756;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)

DE (Endoplasmic reticulum-associated amyloid beta-peptide binding

protein).

GN HADH2 OR HSD17B10 OR ERAB.

OS Mus musculus (Mouse).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA;
RC Fu J., Chen X., Stern D., Yan S.D.;
RC Submitted (Apr-1997) to the EMBL/GenBank/CDJ databases.
CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
CC + NADH.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
CC The European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U96116; AAB57689.1; ALT_INIT.
DR HSSP: O70351; 1E6W.
DR SWISS-2DPAGE: O08756; MOUSE.
DR MGD: MGI:133871; Hsd17b10.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
DR KMO: OX100000000; NAD.
DR NCBIND: 12
DR ACT_SITE: 168
DR SSQ: 261 AA; 27418 MW; 61213BI3E2839D41 CRC64;
SQ
Query Match 87.2%; Score 1137; DB 1; Length 261;
Best Local Similarity 86.6%; Pred. No. 3e-81;
Matches 226; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

```

```

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN (1)
RC SEQUENCE FROM N.A., AND MUTAGENESIS OF LEU-33 AND PHE-120.
RC STRAIN=Canlon-S;
RC MEDLINE=98252852; PubMed=9585418;
RC Torroja L., Ortuno-Sahagun D., Ferrus A., Haemmerle B., Barbás J.A.;
RC "Scully, an essential gene of Drosophila, is homologous to mammalian
RC mitochondrial type II L-3-hydroxyacyl-CoA dehydrogenase/amyloid-beta
RC peptide-binding protein."
RC J. Cell Biol. 141:1009-1018(1998).
RN (2)
RC SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RC MEDLINE=20196006; PubMed=10731132;
RC Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RC Amaratilake P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RC George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RC Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RC Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RC Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RC Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RC Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RC Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,
RC Borrova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RC Butris K.C., Busam D.A., Butler H., Cadenhead L.B., Center A., Chandra I.,
RC Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RC de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RC Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RC Durbin K.J., Evangelista C.C., Ferraz C., Ferrelle S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mervinov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paclik J.M.,
RA Palczkolo M., Plitman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E.G., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkac R., Tector C., Turner R., Ventier E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
Science 287:2185-2195(2000).
CC -1- FUNCTION: MAY PLAY A ROLE IN GERM LINE FORMATION.
CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
CC + NADH.
CC -1- SUBUNIT: MULTIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
CC -1- TISSUE SPECIFICITY: FOUND IN MANY TISSUES INCLUDING CNS, HIGHEST
CC EXPRESSION IN BOTH EMBRYONIC GONADAL PRIMORDIA AND MATURE OVARIES
CC AND TESTES.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
CC The European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: Y15102; CAA75377.1;

```



```

DR EMBL: AE003507; AAF48797.1; -.
DR HSSP; 070351; 1E3W.
DR Flybase; FBgn0021765; scu.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short.1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT.1.
DR Oxidoreductase; NAD; Mitochondrion.
KM NP_BIND 6 31 NAD (BY SIMILARITY).
FT ACT_SITE 162 162 BY SIMILARITY.
FT MUTAGEN 33 33 L->Q: LETHAL ALLELE.
FT MUTAGEN 120 120 F->I: LETHAL ALLELE.
SQ SEQUENCE 255 AA; 26905 MW; F58690643FA0FD03 CRC64;

Query Match 69.6%; Score 908; DB 1; Length 255;
Best Local Similarity 68.9%; Pred. No. 1.6e-63;
Matches 175; Conservative 29; Mismatches 50; Indels 0; Gaps 0;

QY 8 VKGLVAVITGASGLTAERLVGOGASAVLLDIPNSGGEAQAARKLNVCYFADADYTS 67
DB 2 IKNAVSLVTGASGLGRATAEKRLAAGCAVILLADLPSSKGNVAKELGKVFVFEVDYTS 61
QY 68 EKDVQALALAKGEGRVAVNACGIAVASTYNNKGGQTLEDFOEYLDVNLMTGFN 127
DB 62 EKDVSAALQTAEDKFEGRDLTFVNCAGTATVATFENKNVAHRLDEFOEYININTVGTEN 121
QY 128 VTRLVGEVGONPDGOGGORYIINTASVAFEGOGVGAASASGKGIYGMTLPARDLA 187
DB 122 VRLSGKMGANPEPDGOGGVYVNTASVAFEDGQICGAHYASASRAAVGMLPLARDIS 181
QY 188 PIGIRVMTIAPGLFTPLTSLPEKYCNFLASQVPPSPSLGDAPEYAHVQAIIENPFLN 247
DB 182 TGIRICTIAPGLFNPMLALPEKVRTFLAKSIPPPQLGEPSEYAHVQAIVENPFLN 241
QY 248 GEVIRIDGALRMOP 261
DB 242 GEVIRIDGALRMOP 255

RESULT 6
YD50_MYCTU STANDARD; PRT; 247 AA.
ID YD50_MYCTU
AC 011020;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative oxidoreductase RV1350 (EC 1.-.-.-).
GN FABG2 OR RV1350 OR MT1393 OR MTCY02B10.14.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteriales;
OC Actinomycetales; Corynebacteriales; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekla E.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornby T., Jagels K., Krogh J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Omayam L.A., Emdalaeva M.D., Salzberg S.L.,

```

```

RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SCR) FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL; Z75555; CA99983.1; -.
DR HSSP; AE007012; AAK45656.1; -.
DR HSSP; 070351; 1E3S.
DR TIGR; MT1393; -.
DR TubercuList; RV1350; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short.1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT.1.
KM Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
FT NP_BIND 9 34 NAD (BY SIMILARITY).
FT ACT_SITE 155 155 BY SIMILARITY.
SQ SEQUENCE 247 AA; 25871 MW; 76CA07892E7BB9A73 CRC64;

Query Match 29.4%; Score 383.5; DB 1; Length 247;
Best Local Similarity 38.9%; Pred. No. 6.7e-23;
Matches 96; Conservative 43; Mismatches 91; Indels 17; Gaps 5;

QY 13 AVITGASGLGATAEKRLVGVGASAVLLDIPNSGGEAQAARKLNVCYFADADYTSKRD 70
DB 10 AVITGAGAGGLGALGQRFVAGSARVYLDVLEATEVAAKLGGDDVALAARCVYTAQDD 69
QY 71 VQIALALAKGEGRVAVNACGIAVASTYNNKGGQTLEDFOEYLDVNLMTGFN 130
DB 70 VDILIRTAVEREGGADVAVNNAAGITRDATM-----RTMEOPDQVAVAHKGTWGTGR 123
QY 131 LVASGEMGNPDGOGGORYIINTASVAFEGOGVGAASASGKGIYGMTLPARDLAPIG 190
DB 124 LAAATMRER-----KRAIVNMSVSGKVGNGOTNYSKAKGIVGTRAAKAELEHIG 177
QY 191 IRVMTIAPGLFTPLTSLPEKYCNFLASQVPPSPSLGDAPEYAHVQAIIENPFLNG 248
DB 178 IRVNAIAPGLIRSAATEAMPQRIWOKLAIEYPM-GRAGEPEVSAVAVFLASDLSYWTG 236
QY 249 EVIRIDG 255
DB 237 TVLDVVG 243

RESULT 7
FABG_THEMA STANDARD; PRT; 246 AA.
ID FABG_THEMA
AC Q9X248;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
GN FABG OR TM1724.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
OC Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;

```

RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
 RA Haff D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Liner K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequence of *Thermotoga maritima*.";
 RL Nature 393:323-329(1999).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AE001811; AAD36790.1; .
 DR HSSP; P50162; 1AEL.
 DR TIGR; TM124; .
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 10 34 NADP (BY SIMILARITY).
 FT ACT_SITE 154 154 BY SIMILARITY.
 FT SEQUENCE 246 AA; 26401 MW; 8C08904D2809142 CRC64;
 SQ
 Query Match 26.2%; Score 341; DB 1; Length 246;
 Best Local Similarity 33.7%; Pred. No. 1.3e-19;
 Matches 86; Conservative 47; Mismatches 104; Indels 18; Gaps 5;
 QY 8 VKGLAVITGASGLGIATAEERLVGOGASAVLLDLPNSGEA---QAKKLGNNCVAPAD 64
 DB 3 LEGVVCILITGAASIGKATLTLLFAOGATVIADISKENDLSVKEAGELPGKVDYVYN 62
 QY 65 VTSEKDVQTLALAKGFGFVDVAVNACIAVASKYINLKGSTHLEDFORVLDVNLNG 124
 DB 63 VTDROQKEVEKVEKVVQYGRIDVAVNAGITRDALVRMKE-----EDMDAVINVLKG 116
 QY 125 TFNVIRLVAGENGQNEPDGQGRVLIINTASVAEFGVQQAIVSASKGIVMTPIAR 184
 DB 117 VFNVTQWVAVYMKQ-----RNGSIVNASSVVGIGNPGQITVYASKMGVIGMTTK 170
 QY 185 DLAPIGRTVITAGLFGTPLITSLEPKVCNFIASQVPPFSKIGDAEVAHLV--QALIE 242
 DB 171 ELGGRNIRVNAVAPGFIETETKELEPKARETALSRIPL-GRGKPEEVAOVILLFLASDE 229
 QY 243 NPELNGEVRILDGAI 257
 DB 230 SSYVTGGVIGIDGL 244
 RESULT 8
 DH88_HUMAN STANDARD; PRT; 261 AA.
 AC Q92506; O9UI01;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Estradiol 17 beta-dehydrogenase 8 (EC 1.1.1.62) (17-beta-HSD 8) (17-
 DE beta-hydroxysteroid dehydrogenase 8) (K6 protein) (K6-6).
 GN HSD17B8 OR HEB2 OR RING2 OR FABG1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RP Tubbey B.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RP [2]
 RP SEQUENCE OF 3-261 FROM N.A.
 RX MEDLINE=97001166; PubMed=8812499;
 RA Ando A., Kikuli Y.Y., Shigenari A., Kawata H., Okamoto N., Shina T.,
 RA Chen L., Ikemura T., Ade K., Kimura M., Inoko H.;
 RT cDNA cloning of the human homologues of the mouse K64 and K66 genes
 RT at the centromeric end of the human MHC region.";
 RL Genomics 35:600-602(1996).
 CC -1- FUNCTION: USES ESTRADIOL AS ITS PREFERRED SUBSTRATE.
 CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P)(+) = estrone +
 CC NAD(P)H.
 CC -1- PATHWAY: BIOSYNTHESIS OF ESTROGENS.
 CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE LIVER AND PANCREAS,
 CC LOWER IN THE SKELETAL MUSCLE AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AL031228; CAC38444.1; .
 DR EMBL; D82061; BA111529.1; .
 DR HSSP; 070351; 1E6W.
 DR Genew; HGNC:3554; HSD17B8.
 DR MIM: 601417; .
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR Steroid biosynthesis; Oxidoreductase; NAD; Multigene family.
 KW NP_BIND 15 39 NAD (BY SIMILARITY).
 FT ACT_SITE 169 169 E -> R (IN REF. 2).
 FT CONFLICT 117 117 E -> P (IN REF. 2).
 FT CONFLICT 193 193 R -> P (IN REF. 2).
 FT CONFLICT 208 208 Q -> K (IN REF. 2).
 FT CONFLICT 212 212 Q -> K (IN REF. 2).
 FT SEQUENCE 261 AA; 26974 MW; 8BBB2D7131714D71 CRC64;
 SQ
 Query Match 25.6%; Score 334; DB 1; Length 261;
 Best Local Similarity 31.0%; Pred. No. 4.9e-19;
 Matches 85; Conservative 55; Mismatches 106; Indels 28; Gaps 8;
 QY 1 MAAYVS-VKGLAVITGASGLGIATAEERLVGOGASAVLLDLPNSGEAQAQKTI----- 54
 DB 1 MASOLQNRRLRSALAVLTGASGIGRAVSRLRGEATVAACDLDRAAQAQETVRLRGGGS 60
 QY 55 -----GNVCVAPADVSEKDVQFALALAKGFGFVDVAVNACIAVASKYINLKGQ 107
 DB 61 KEGPPRGNHAF-QADVSEARAARCLLEQVACFSRPSVYVSCGIIODEFLHMSG-- 117
 DB 118 ----DDMDVIAVNEKGFVLVQAAQALVSN-----CGRGSIIINISSIVGKGVNGQTN 168
 QY 168 VSASKGIVGMLPLFARDLAPIGIRVMTIAPGLFTPLITSLEPKVCNFIASQVPPFSRL 227
 DB 169 YASKRAGVIGLQTLARELGRHICNSVLPFIATPMQKVPKVVADKITEMPM-GHL 227
 QY 228 GDPAEVAHLVQ--AIENPFLNGEVRILDGAI 259
 DB 228 GDPEDVADVAVFLASEDSGYIITGSEVTGGLEW 261

RESULT 9
FABG_CUPLA STANDARD; PRT; 320 AA.
ID FABG_CUPLA
AC P28643;
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 40, Last annotation update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase, chloroplast precursor
DE (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
GN CLKR27.
OS Cuphea lanceolata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Myrtaceae; Cuphea.
OX NCBI_Taxid=3930;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92293104; PubMed=1376402;
RA Klein B., Pawlowski K., Hoerlcke-Grandpierre C., Scheil J.,
RA Toepfer R.;
RT Isolation and characterization of a cDNA from Cuphea lanceolata
RT encoding a beta-ketoacyl-ACP reductase.";
RL Mol. Gen. Genet. 233:122-128(1992).
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC PATHWAY.
CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC
CC PLASTIDS.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X64566; CAA45866.1; -
DR PIR: S19832; S19832.
DR HSSP: P50162; 1AEL.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT.1.
KM Fatty acid biosynthesis; Oxidoreductase; NADP; Chloroplast;
KM Transit peptide.
FT TRANSIT 1 61 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 62 320 3-OXOACYL-[ACYL-CARRIER PROTEIN]
FT FT 62 320 REDUCTASE.
FT NR_BIND 82 106 NADP (BY SIMILARITY).
FT ACT_SITE 227 227 BY SIMILARITY.
SQ SEQUENCE 320 AA; 33103 MW; 06BAF0522B8C87 CRC64;
Query Match 25.6%; Score 334; DB 1; Length 320;
Best Local Similarity 32.7%; Pred. No. 6.2e-19;
Matches 87; Conservative 46; Mismatches 111; Indels 22; Gaps 6;

QY 2 AAATSVKGLVAVITGASGLATATRLVVGOGASAVLLDLPNSGGEA-----QAKKLN 56
DB 69 AGAGSVSPVIVITGASRGIGKAIKALSL-GRAGCKVLVYVARSKEAEVSKREIDAFGG 127
QY 57 NCYFAPADVTSEKDVQTALALAKGKGRVDVAVNCGIAVASTYLNKKGQTTLEDPR 116
DB 128 QALTFGGDSKEDVEKMTITAVDANGVTIDILNNAGITRDGLMKRKSQ-----WGE 181
QY 117 VLDVNLGTFNVLRLVAGENGQNEPDGQGGVYIINTASVAEFGGVGQAASASKGGIV 176
DB 182 VIDNLTLGVFLCQAQAKIMKK-----KKRITINIASVYGLVGNAGQANVSAAKAGVI 235

QY 177 GKTLPIADLAPIGIRVWTIPGCFGPIILSLPEKVCNPLASGVPPSRRLGDAEAYHL 236
DB 236 GFTKTVAREYASRNINWNAVAPGISDPMKSLDIDINKLLETIPL-GRYGPPEVAVGL 294
QY 237 VOALIEPN---FLNGEVIRLDGALRM 259
DB 295 VEFALNPASSVYTGCVFTIDGKTM 320

RESULT 10
FABG_VIBCH STANDARD; PRT; 244 AA.
ID FABG_VIBCH
AC Q9KOH7;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
GN FABG OR VC2021.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_Taxid=666;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae".
RL Nature 406:477-483(2000).
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE004276; AAF95169.1; ALT_INIT.
DR HSSP: P19992; IHDC.
DR TIGR: VC2021; -
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT.1.
KM Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
KM NP_BIND 10 34 NADP (BY SIMILARITY).
FT ACT_SITE 151 151 BY SIMILARITY.
SQ SEQUENCE 244 AA; 25566 MW; 9FB2E8278B7C3CE CRC64;
Query Match 25.2%; Score 328.5; DB 1; Length 244;
Best Local Similarity 32.0%; Pred. No. 1.2e-18;
Matches 82; Conservative 54; Mismatches 103; Indels 17; Gaps 5;

QY 7 SVKGLVAVITGASGLATATRLVVGOGASAVLLDLPNSGGEAQAQKKGNCVAPADVT 66
DB 2 NIEGRVAVITGASRGIGKAIKALSL-GRAGCKVLVYVARSKEAEVSKREIDAFGG 61
QY 67 SKDVQTALALAKGKGRVDVAVNCGIAVASTYLNKKGQTTLEDPRVLDVNLGTF 126

```

Db      62 NPSIAVAVKATIDEGVDILVNNAGITRDNLKMKK-----EEMSDIETITLSTIF 115
Qy      127 NYRLVAGMGVGNPDGOGVGIINTASVAFEGOVGAASASGKIVGTLPILARDL 186
Db      116 RLKSKAVLRGMKK-----RGRITVGSVGTGKGNAGANAAKAGVIGTKMARREV 169
Qy      187 APGIVMTAPGLFCTPLTSLPEKVCNPLASQVFPSPRLCDPAEYAHVQAITIENP-- 244
Db      170 ASRGVYVNTVAPGFITDITDKALINDEORTATLQVAP-AGRLDDPREIASAV-AFLASPEA 227
Qy      245 -FLNGEVIRLDGAIRM 259
Db      228 AITGETLHVNGMVM 243

RESULT 11
DH88_MOUSE STANDARD: PRT: 260 AA.
AC PS0171: Q60959; Q60958; Q921W2;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Estradiol 17 beta-dehydrogenase 8 (EC 1.1.1.62) (17-beta-HSD 8) (17-
DE beta-hydroxysteroid dehydrogenase 8) (Ke6 protein) (Ke-6).
GN HSD17B8 OR HKE6 OR H2-KE6.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Kidney;
RX MEDLINE=93180832; PubMed=8441417;
RA Aziz N., Maxwell M.M., St Jacques B., Brenner B.M.;
RT "Downregulation of Ke 6, a novel gene encoded within the major
RT histocompatibility complex, in murine polycystic kidney disease.";
RL Mol. Cell. Biol. 13:1847-1853(1993).
RN [2]
RP ERRATUM.
RA Aziz N., Maxwell M.M., St Jacques B., Brenner B.M.;
RL Mol. Cell. Biol. 13:6614-6614(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=96027630; PubMed=7559658;
RA Maxwell M.M., Nearing J., Aziz N.;
RT "Ke 6 gene. Sequence and organization and aberrant regulation in
RT murine polycystic kidney disease.";
RL J. Biol. Chem. 270:25213-25219(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RA Rowen L., Qin S., Madan A., Loretz C., James R., Dors M., Mix L.,
RA Hall J., Lasky S., Hood L.;
RT "Sequence of the mouse major histocompatibility locus class II
RT region.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: USES ESTRADIOL AS ITS PREFERRED SUBSTRATE.
CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P)(+) = estrone +
CC NAD(P)H.
CC -1- PATHWAY: BIOSYNTHESIS OF ESTROGENS.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A SHORT FORM (SHOWN HERE) AND A
CC LONG FORM: ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: KIDNEY, LIVER AND MODERATELY IN SPLEEN, HEART
CC AND BRAIN.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U34072: AAC53573.1; -
CC CC EMBL: U34072: AAC53574.1; -
DR EMBL: AF100956; AAC69902.1; -
DR HSSP: 070351; 1E6W.
DR MGD: MGI:95911; H2-Ke6.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Steroid biosynthesis; Oxidoreductase; NAD; Multigene family;
KM Alternative splicing.
FT NP_BIND 13 38 NAD (BY SIMILARITY).
FT ACT_SITE 168 168 BY SIMILARITY.
FT VARSPIC 257 260 GLFM -> MRPSMGGOENRQVYMRK (IN LONG
FT ISOFORM).
FT CONFLICT 16 16 G -> GSGVPSQ (IN REF. 3).
FT CONFLICT 17 17 MISSING (IN REF. 1).
FT CONFLICT 230 230 E -> EG (IN REF. 1).
SQ SEQUENCE 260 AA; 26645 MW; 19C712FCD168B08 CRC64;

Query Match 24.2%; Score 315.5; DB 1; Length 260;
Best Local Similarity 31.0%; Pred. No. 1.3e-17;
Matches 85; Conservative 55; Mismatches 105; Indels 29; Gaps 9;

Qy 1 MAAVRSKGLVAVITGGA-SGLGLATNRERYVGGAGANALIDLPNSGGEAOKLGN--- 56
Db 1 MASQLR-LRSALVALVTGAGSGIGRAISVRLAAGAAVAACDLDGAAQDVRLLSGPGS 59
Qy 57 -----NCVFAPADVTSEKDVOTATALAKGKFR-VDVAVNCAGIAVASKTYNLRKQ 107
Db 60 EDGARPKGHAF-QADVSQGPAAARLLLEVQACSRFPSSVYVSCAGITRDEFLHME-- 116
Qy 108 THTLEDFOVLDVNLGTFNVIYRLVAGMGVGNPDGOGVGIINTASVAFEGOVQGA 167
Db 117 ---EDMDRVAVNWKGFVLVTOAAQALVSS-----GGRSIIINISIIIGKVNIGQTN 167
Qy 168 YSASKGIVGMLTPIARDLPIGIRVMTAPGLFCTPLTSLPEKVCNPLASQVFPSPRL 227
Db 168 YASSAGVIGLQNRARLGRNCRNSVLPGLFATIPQTMKPRKVDKVTAMPL-GHM 226
Qy 228 GDPAEYAHVQ--ATTENPFLNGEVIRLDGAIRM 259
Db 227 GDPEDVADVAVAFELASEDSGYITGASVEVSGGLFM 260

RESULT 12
PAG1_SYNY3 STANDARD: PRT: 247 AA.
ID PAG1_SYNY3
AC P73574;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-l-acyl-carrier protein reductase 1 (EC 1.1.1.100) (3-
DE ketoacyl-acyl carrier protein reductase 1).
GN FABG1 OR SLR086.
OS Synchocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asanizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugita W., Sasamoto S., Kimura I.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nario K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).

```


Db 61 APADVTSEKDVOTATLALAKGKFRVDVAVNACAGIAVASRTYVLLKKGGTHLEDFORVLDV 120
QY 121 NMGTFNVIRLVAGGKQNEPPOGGORGIITNTASVAAFEQVGAATASASNGIVGML 180
Db 121 NMGTFNVIRLVAGGKQNEPPOGGORGIITNTASVAAFEQVGAATASASNGIVGML 180
QY 181 PIARDLAPIGIRMTIAPGLFGTPLTSLPEKVCNFLASQVFPSPRLGDPAPAEYAHVQAI 240
Db 181 PIARDLAPIGIRMTIAPGLFGTPLTSLPEKVCNFLASQVFPSPRLGDPAPAEYAHVQAI 240
QY 241 IENPFLNGEYIRLDGAI RMQP 261
Db 241 IENPFLNGEYIRLDGAI RMQP 261

RESULT 6

US-09-931-186-2
Sequence 2, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELVIN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AGREST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOMALTER, RICHARD E.
APPLICANT: TEMPALZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/RAD2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
TITLE OF INVENTION: OF INHIBITORS THEREOF
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214R
US-09-931-186-2

Query Match 98.7%; Score 1287; DB 10; Length 261;
Best Local Similarity 99.2%; Pred. No. 1,1e-108;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MAASVSKGLVAVITGASGLGLATAERLVGGASAVLLDLPNSGGEQAOKLGNCF 60
Db 1 MAASVSKGLVAVITGASGLGLATAERLVGGASAVLLDLPNSGGEQAOKLGNCF 60
QY 61 APADVTSEKDVOTATLALAKGKFRVDVAVNACAGIAVASRTYVLLKKGGTHLEDFORVLDV 120
Db 61 APADVTSEKDVOTATLALAKGKFRVDVAVNACAGIAVASRTYVLLKKGGTHLEDFORVLDV 120
QY 121 NMGTFNVIRLVAGGKQNEPPOGGORGIITNTASVAAFEQVGAATASASNGIVGML 180
Db 121 NMGTFNVIRLVAGGKQNEPPOGGORGIITNTASVAAFEQVGAATASASNGIVGML 180
QY 181 PIARDLAPIGIRMTIAPGLFGTPLTSLPEKVCNFLASQVFPSPRLGDPAPAEYAHVQAI 240
Db 181 PIARDLAPIGIRMTIAPGLFGTPLTSLPEKVCNFLASQVFPSPRLGDPAPAEYAHVQAI 240
QY 241 IENPFLNGEYIRLDGAI RMQP 261
Db 241 IENPFLNGEYIRLDGAI RMQP 261

RESULT 7

US-09-984-245-245
Sequence 245, Application US/09984245
Patent No. US20020165374A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
CURRENT APPLICATION NUMBER: US/09/984,245
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/05311
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: US 60/041,277
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/042,344
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,276
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,281
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/048,094
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,350
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,188
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,135
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/050,937
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,187
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,099
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,352
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,186
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,069
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,095
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,131
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,096
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,355
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,160
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,351
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/060,862
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 245
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-09-984-245-245

Query Match 87.9%; Score 1146; DB 9; Length 227;

Thu Jun 26 06:55:08 2003

us-09-931-186-4.rapb

Page 5

Best Local Similarity 100.0%; Pred. No. 5,1e-96;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 ASAVLLDLPNSGGEQAOKKLGNNCYFAPADYTSKDVQTALALAKGFGRYDVAVNCAGI 94
DB 1 ASAVLLDLPNSGGEQAOKKLGNNCYFAPADYTSKDVQTALALAKGFGRYDVAVNCAGI 60
QY 95 AVASKTYNLKKGQHTLEDFOFVLDVNLMTGFNVIRLVAGMGONEPDGGGQGVYIINTA 154
DB 61 AVASKTYNLKKGQHTLEDFOFVLDVNLMTGFNVIRLVAGMGONEPDGGGQGVYIINTA 120
QY 155 SVAAFEGQVGOAAYASASKSGIVGNTLPFARDLAPIGIVMTIAPGLFGTPLTSLPEKVC 214
DB 121 SVAAFEGQVGOAAYASASKSGIVGNTLPFARDLAPIGIVMTIAPGLFGTPLTSLPEKVC 180
QY 215 NFLASQVPPPSRLGDPAEYAHLYVQAIIENPFNGEVIIRLDGAIIRMQP 261
DB 181 NFLASQVPPPSRLGDPAEYAHLYVQAIIENPFNGEVIIRLDGAIIRMQP 227

RESULT 8
US-09-966-262-245
; Sequence 245, Application US/09966262
; Publication No. US20030050461A1
GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/966,262
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: US 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351

QY 35 ASAVLLDLPNSGGEQAOKKLGNNCYFAPADYTSKDVQTALALAKGFGRYDVAVNCAGI 94
DB 1 ASAVLLDLPNSGGEQAOKKLGNNCYFAPADYTSKDVQTALALAKGFGRYDVAVNCAGI 60
QY 95 AVASKTYNLKKGQHTLEDFOFVLDVNLMTGFNVIRLVAGMGONEPDGGGQGVYIINTA 154
DB 61 AVASKTYNLKKGQHTLEDFOFVLDVNLMTGFNVIRLVAGMGONEPDGGGQGVYIINTA 120
QY 155 SVAAFEGQVGOAAYASASKSGIVGNTLPFARDLAPIGIVMTIAPGLFGTPLTSLPEKVC 214
DB 121 SVAAFEGQVGOAAYASASKSGIVGNTLPFARDLAPIGIVMTIAPGLFGTPLTSLPEKVC 180
QY 215 NFLASQVPPPSRLGDPAEYAHLYVQAIIENPFNGEVIIRLDGAIIRMQP 261
DB 181 NFLASQVPPPSRLGDPAEYAHLYVQAIIENPFNGEVIIRLDGAIIRMQP 227

Query Match 87.9%; Score 1146; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 5,1e-96;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 ASAVLLDLPNSGGEQAOKKLGNNCYFAPADYTSKDVQTALALAKGFGRYDVAVNCAGI 94
DB 1 ASAVLLDLPNSGGEQAOKKLGNNCYFAPADYTSKDVQTALALAKGFGRYDVAVNCAGI 60
QY 95 AVASKTYNLKKGQHTLEDFOFVLDVNLMTGFNVIRLVAGMGONEPDGGGQGVYIINTA 154
DB 61 AVASKTYNLKKGQHTLEDFOFVLDVNLMTGFNVIRLVAGMGONEPDGGGQGVYIINTA 120
QY 155 SVAAFEGQVGOAAYASASKSGIVGNTLPFARDLAPIGIVMTIAPGLFGTPLTSLPEKVC 214
DB 121 SVAAFEGQVGOAAYASASKSGIVGNTLPFARDLAPIGIVMTIAPGLFGTPLTSLPEKVC 180
QY 215 NFLASQVPPPSRLGDPAEYAHLYVQAIIENPFNGEVIIRLDGAIIRMQP 261
DB 181 NFLASQVPPPSRLGDPAEYAHLYVQAIIENPFNGEVIIRLDGAIIRMQP 227

RESULT 9
US-09-983-966-245
; Sequence 245, Application US/09983966
; Publication No. US20030060619A1
GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/983,966
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099

PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,352
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,186
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,069
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,095
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,131
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,096
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,355
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,160
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,351
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,154
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/054,804
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/056,370
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: US 60/060,862
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 245
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-09-983-966-245

Query Match
Best Local Similarity 100.0%; Score 1146; DB 9; Length 227;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 ASAYLLDLPNSGGEQAQKLGNNCFAPADVTSEKDVOTALALAKGFGVAVVNCAGI 94
DB 1 ASAYLLDLPNSGGEQAQKLGNNCFAPADVTSEKDVOTALALAKGFGVAVVNCAGI 60
QY 95 AVASKTYNLKKGGOTHTLEDFQFVLDVNLGTFENVIRLVAGEMGONEDDGGORGVIIINTA 154
DB 61 AVASKTYNLKKGGOTHTLEDFQFVLDVNLGTFENVIRLVAGEMGONEDDGGORGVIIINTA 120
QY 155 SVAAFEGVGOAAYASASKGIVGMLPIARDLAPIGIRVMTIAPGLFTPLTSLPERVC 214
DB 121 SVAAFEGVGOAAYASASKGIVGMLPIARDLAPIGIRVMTIAPGLFTPLTSLPERVC 180
QY 215 NFLASQVFPFSLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKMP 261
DB 181 NFLASQVFPFSLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKMP 227

RESULT 10
US-10-143-090-245
Sequence 245, Application US/10143090
Publication No. US20030069406A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
CURRENT APPLICATION NUMBER: US/10/143,090
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 245
LENGTH: 227
TYPE: PRT

ORGANISM: Homo sapiens
US-10-143-090-245

Query Match
Best Local Similarity 100.0%; Score 1146; DB 9; Length 227;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 ASAYLLDLPNSGGEQAQKLGNNCFAPADVTSEKDVOTALALAKGFGVAVVNCAGI 94
DB 1 ASAYLLDLPNSGGEQAQKLGNNCFAPADVTSEKDVOTALALAKGFGVAVVNCAGI 60
QY 95 AVASKTYNLKKGGOTHTLEDFQFVLDVNLGTFENVIRLVAGEMGONEDDGGORGVIIINTA 154
DB 61 AVASKTYNLKKGGOTHTLEDFQFVLDVNLGTFENVIRLVAGEMGONEDDGGORGVIIINTA 120
QY 155 SVAAFEGVGOAAYASASKGIVGMLPIARDLAPIGIRVMTIAPGLFTPLTSLPERVC 214
DB 121 SVAAFEGVGOAAYASASKGIVGMLPIARDLAPIGIRVMTIAPGLFTPLTSLPERVC 180
QY 215 NFLASQVFPFSLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKMP 261
DB 181 NFLASQVFPFSLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKMP 227

RESULT 11

US-09-920-923-41
Sequence 41, Application US/09920923
Publication No. US20030022273A1
GENERAL INFORMATION:

APPLICANT: Pasamontes, Luis
APPLICANT: Isyankov, Yuri
TITLE OF INVENTION: Improved Fermentative Carotenoid Production
FILE REFERENCE: Improved Fermentative Carotenoid
CURRENT APPLICATION NUMBER: US/09/920,923
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 08/980,832
PRIOR FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41
LENGTH: 388
TYPE: PRT
ORGANISM: Flavobacterium sp. R1534
US-09-920-923-41

Query Match
Best Local Similarity 51.0%; Score 664.5; DB 9; Length 388;
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VKGLVAVITGGASGLATAEKLVGOGASAVLLDLPNSGGEQAQKLGNNCFAPADVT 67
DB 143 IEGRVTVVIGASGLGASRMLAOGGAKVTLADL-----AEPKAPRGVHAACDVID 196
QY 68 EKDVQATALAKGFGVAVVNCAGI AVASKTYNLKKGGOTHTLEDFQFVLDVNLGTFN 127
DB 197 ATAQATATATDREFGRDLGVNCAGIAPAEKV--LGRGPGIGLDSFAVAVTINIGSPN 254
QY 128 VIRLVAGEMGONEDDGGORGVIIINTASVAAFEGVGOAAYASASKGIVGMLPIARDL 187
DB 255 MARLAAPAMAKRNPVR-GERGVIVNTASTAODGQIGQVAYIASKAGVAGKMLLPANRDA 313
QY 188 PIGIRVMTIAPGLFTPLTSLPERVCNFLASQVFPFSLGDPAEYAHVQAIIENPFLN 247
DB 314 RHGIRVMTIAPGLFTPLTSLPERVCNFLASQVFPFSLGDPAEYAHVQAIIENPFLN 373
QY 248 GEVIRLDGAIKMP 261
DB 374 GEVIRLDGAIKMP 387

RESULT 12
US-09-931-186-17
Sequence 17, Application US/09931186

```

; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: ABREO, MELVIN A.
; APPLICANT: AGREE, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REUTO, PAUL A.
; APPLICANT: SHOWALTER, RICHARD E.
; APPLICANT: THOMSON, JIM
; APPLICANT: TEMPCZYK-RUSSELL, ANNA
; APPLICANT: VANDERPOOL, DARIN
; APPLICANT: VILLAFRANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
; TITLE OF INVENTION: OF INHIBITORS THEREOF
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931,186
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 17
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-931-186-17

Query Match      25.5%; Score 332.5; DB 10; Length 259;
Best Local Similarity 31.2%; Pred. No. 2.3e-22;
Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;

QY 8 VGLVAVITGASGLATAEERLVGQASAVLLDLPNSGGGAQAKL-----GN 56
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 7 LLSALATLVGAGSGIGRAVSVRLAGEGATVACDDIDRAAAGTVALLGPGSKGPPRGN 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 NCVFAPADVTSEKDVDTALALAKKFGF-VDAVAVCAGIAVASKTYNLKKGOTHTLEDFQ 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 67 HAAF-QADVSEARAACLEGVQACSRPPSVVSCAGITODEFLLHSE-----DWD 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 RYLVNLMGTFNVRILVAGEMGONPDGGRGVLIINTASVAAPFEGVGOAAYSASAKGI 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 120 KTVAVNLKGTFLVTAQAQALVSN-----GCRGSIINISSIVGKYNGQTVYASAKAGV 174
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 VGMTLPARDLAPIGIRVNTIAPGLFTPLTSLEPKVONFLASQVPPFSRIGDPAEYAH 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 175 IGLTQTAARELGHRGICNSVLPGLFIAPMTQKVPQKVDKITEMIPM-GRIGDPEDEVAD 233
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 236 LVQ--AIENPFLNGEVIRLDGAIRM 259
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 234 VVAFLASEDSGYITGTSVEVTGLFW 259
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-09-815-242-13360
; Sequence 13360, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078

```

```

; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 13360
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-09-815-242-13360

Query Match      25.0%; Score 326.5; DB 10; Length 243;
Best Local Similarity 35.1%; Pred. No. 7.3e-22;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

QY 15 ITGASGLGATAEERLVGQASAVLLDLPNSGGE-----AQAKKLGNNCVFAPADVTSE 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 10 ITGSSRGIGLAIARFQAQGANIVL---NSRGAISELLAEFSNGIKVVPISGDVSDF 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 69 KDVOATALALAKKFGFGRVAVANCAGIAVASKTYNLKKGOTHTLEDFORVLDVNLGTFNV 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 66 ADARKMIDQAEIAGSVDLVNNNGI---TQDTLMKN---TEADFEKVKLVNLTGAFNM 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 IRLVAGEMGONPDGGRGVLIINTASVAAPFEGVGOAAYSASAKGIAGTLPARDLAP 168
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 120 TQSVL-----KPMKAREGAIINMSSVVGIMNGICANYASAKAGLIGFTKSVAREVAS 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 189 IGIRVNTIAPGLFTPLTSLEPKVONFLASQVPPFSRIGDPAEYAHVIAIENPFLNG 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 174 RNVAVNYIAPMISDMTALISDKIKERTLAQIYM-KEFGQAEVADLTVPFAGQDYLIG 232
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 EVIRLDGAIRM 259
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 233 QVIAIDGGLSM 243
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-09-815-242-13581
; Sequence 13581, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625

```


Thu Jun 26 06:55:08 2003

us-09-931-186-4.rapp

Page 10

```
; TYPE: PRT
; ORGANISM: Bacillus megaterium
; US-09-479-040-9

Query Match
  23.1%; Score 301; DB 9; Length 247;
Best Local Similarity 29.1%; Pred. No. 1.5e-19;
Matches 78; Conservative 59; Mismatches 93; Indels 38; Gaps 9;

QY 7 SVKGLVAVITGASGLGATLAEKLVGQ-----ASAVLLDLPNSGGEAQAOKK 53
DB 3 TLQGVAVITGSGKIGALITRELSNGKAVANVNSKESAEAIYKEIKDNGEA---- 58

QY 54 LGNCFAPADYSESDVGTALALAKGKRGVDVAVNCAGIYASVSTYLRK-GQTHILE 112
DB 59 -----IAVQADVSYDQAKHLIETNAAGOLDILVNNAGI--TRDRSEFKLGE---E 106

QY 113 DFGRLDVNLMGTFNIVRLVAGMGQNEPDGQGRGVIINTASVAFEGVQAAYASAK 172
DB 107 DMKVIDVNLHSYNTSALFHLSE---GGR--VINISSIIGAGGFGQTVYSAX 160

QY 173 GGIYVMTPLIARDLAPIGIRVMTIAPGLTGLTSLPKYCNFLASQVFPFSRLGDPRE 232
DB 161 AGMLGFTKSLALBLATGVTVAIICPGFETEKVMAIPEDVRAKIVAKIP-TRRIGHAE 219

QY 233 YAH-LVQAIENPFNGEVIIRLDGAI 259
DB 220 IARGVYILAKDGAVITGQQLNTINGLYM 247

RESULT 20
US-09-773-748-1
; Sequence 1, Application US/09773748
; Publication No. US20020187537A1
; GENERAL INFORMATION:
; APPLICANT: Wada, Masaru
; TITLE OF INVENTION: Levodione reductase gene and use thereof
; FILE REFERENCE: Levodione reductase
; CURRENT APPLICATION NUMBER: US/09/773,748
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: EP00101665.8
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Corynebacterium aquaticum
; US-09-773-748-1

Query Match
  22.5%; Score 293.5; DB 9; Length 267;
Best Local Similarity 31.8%; Pred. No. 8e-19;
Matches 84; Conservative 45; Mismatches 98; Indels 37; Gaps 9;

QY 12 VAVITGASGLGATLAEKLVGQASAVLLDLPNSGGEAQAOKKLVNCCVAP----ADVT 66
DB 15 VVLTGGSGSLGRATVRLAEGAKSLVDVSESGEASKAAVLETAPAEVYLTIVADS 74

QY 67 SEDVGTALALAKGKRGVDVAVNCAGIYASVSTYLRK-GQTHILEDPQRLDVNLMGTF 126
DB 75 DEQVENVYATATERGRIDGFNNAGIEGQ-----NPESTTALEFKVYSINRGVF 129

QY 127 ----NIVRLVAGMGQNEPDGQGRGVIINTASVAFEGVQAAYASAKSGIYVMTLP 182
DB 130 LGLEKVLKIR-----EAGS--GMVYNTASVCGIRIDGNSGYAAAKHGVYGLTRNS 179

QY 183 ARDLAPIGIRVMTIAPGLTGLTSL-----PEKVC-NFLASQVFPFSRLGDPRE 233
DB 180 AVEYGRKIRINLAIGALITPVEVSMKOLDENFRKAAEFTI--QVNPSCRKRYGAPPI 237

QY 234 AHLVQAIEN--PFLNGEVIIRLDG 255
DB 238 AAVYAFILSDASVAVNATVYPIDG 261
```

```
RESULT 21
US-10-307-385-6
; Sequence 6, Application US/10307385
; Publication No. US20030077797A1
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, MASAKAZU
; APPLICANT: TONOUCHI, NAOTO
; APPLICANT: SUZUKI, SHUNICHI
; APPLICANT: YOKOZEKI, KENZO
; TITLE OF INVENTION: XYLITOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
; FILE REFERENCE: 0010-1024-0
; CURRENT APPLICATION NUMBER: US/10/307,385
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US/09/363,189
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: JP10-216047
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Gluconobacter oxydans
; US-10-307-385-6

Query Match
  22.4%; Score 292.5; DB 9; Length 262;
Best Local Similarity 31.6%; Pred. No. 9.6e-19;
Matches 86; Conservative 41; Mismatches 110; Indels 35; Gaps 7;

QY 6 RSVKGLVAVITGASGLGATLAEKLVGQASAVLLDLPNSG---GEAQAOKKLVNCCVAP 62
DB 3 KFNKGVCLVTVGAGGNIGLATRLAEBGTALIDMNRLEKAEASVREKVEARSYV 62

QY 63 ADVTSEKVPQALALAKGKRGVDVAVNCAGIYASVSTYLRK-GQTHILEDPQRLDVN 122
DB 63 CDVTESEAVIGTVDSVVDGKIDPLFNNAIYQGA-----FAPYQDIPSDDFARVLTINV 117

QY 123 MGFENVIRLVAGEM-GQNEPDGQGRGVIINTASVAFEGVQAAYASAKSGIYVMTLP 181
DB 118 TGAHFVHLKAVSRQMTQN-----YGRIVNTASWAGVKGPPNAAAGASGALITALET 170

QY 182 IARDLAPIGIRVMTIAPGLTGLTSLPKYCNFLASQVFPFSRLGDPRE 225
DB 171 AALDLAPYINIRYNALSPGYMGPGFEMWKEQVELQAKVSGQYSTDPRKYVAQOMIGSVPR-R 229

QY 226 RLGDPAEYVAHLVQAIEN--ENPFNGEVIIRLDG 255
DB 230 RYGDINEIRGVYAFILGDDSSFMGMGVNPIAG 261

RESULT 22
US-09-802-853-6
; Sequence 6, Application US/09802853
; Patent No. US20010034049A1
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, MASAKAZU
; APPLICANT: TONOUCHI, NAOTO
; APPLICANT: SUZUKI, SHUNICHI
; APPLICANT: YOKOZEKI, KENZO
; TITLE OF INVENTION: XYLITOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
; FILE REFERENCE: 0010-1024-0
; CURRENT APPLICATION NUMBER: US/09/802,853
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 09/363,189
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: JP10-216047
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 262
; TYPE: PRT
```

ORGANISM: Gluconobacter oxydans
US-09-802-853-6

Query Match 22.4%; Score 292.5; DB 10; Length 262;
Best Local Similarity 31.6%; Pred. No. 9, 6e-19;
Matches 86; Conservative 41; Mismatches 110; Indels 35; Gaps 7;

QY 6 RSVKGLVAVITGASGLGATATERYLVGGASAVLDLPNSG---GSAQKRLGNVCVAF 62
DB 3 KKEKNGVCLVTGAGGIGGATRLRLAEETALALDMDNEALEKRAEASREKGVARSIV 62
QY 63 ADYTSKEDVQOTALALAKKFRDYDAVAVNAGIAVASKYVNLKKGQTHLTEDFORVLDVNL 122
DB 63 CDVTSEAVIGIVDSVVRDFGKIDFLFNAGYOGA----FAPVODPSDDPFRVLTIV 117
QY 123 MGFENYIRLVAGEM-GQNEPDGQGRGVITINTASVAFEGVGOAAYSASKGIYGMFLP 181
DB 118 TGAFLIKAVSRMTQN-----YGRIVNTRASNAGVGPNNMAAYGSKAIIALTET 170
QY 182 IARDLAPIGIRVNTIAPGLF-----GTPDLTSLPEKYCNFLASOVPPS 225
DB 171 AALDLAPYINRYVAISPGYMGPFMERQVELQAKVGSYFSTDPVVAQOMIGSVPM-R 229
QY 226 RLGDPRVAHLVQAII--ENPFLNGEVIPLDG 255
DB 230 RYGDINIEPGVAFELGDDSSFTGTGNLPIAG 261

RESULT 23

US-09-978-295A-468
Sequence 468, Application US/09978295A
Patent No. US20020156006A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978, 295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819

Thu Jun 26 06:55:08 2003

us-09-931-186-4.rapb

Page 12

PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085333
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 22.4%; Score 291.5; DB 9; Length 270;
Best Local Similarity 31.7%; Pred. No. 1.2e-18;
Matches 86; Conservative 42; Mismatches 106; Indels 37; Gaps 8;

QY 1 MAAVRSVKGLVAVITGASGLATAEPLVGGASAVLDLPNSGGEAQRKGNVCF 60
DB 1 MATGER-YAKGVYVYVGGGRIGAGIVAFVNSGARVYIDCKDESGGRLAECEL-DGAYF 58
QY 61 APADVTSEKDYORALAKGKFGFVAVVAVCAGIYASAKYNNKKGQTHLEDFORVLDV 120
DB 59 ILCDVTGEDVDYKTLVSETIRFRGLDCVNNAGHPPP-----QREETSAGFRULEL 113
QY 121 NMGTFVYIRLVAGEMQNEPDGQGRVYIINTASVAAPFGQVGOAAVSASKGIYGMTL 180
DB 114 NLGTYTLTKLALPYLKSQ-----GNVINISLVGAIGQAQVYVATKGAVTAMK 166
QY 181 PIARDLAPIGIRWTTIPAGFGTPILTSLPEKCNFLASVPPP-----SRL 227
DB 167 ALADESPYGVKVCISPGNINWTPMBE-----LAALMPFRATIRGMLAQLPGRM 218
QY 228 GDPAEY-AHLVQATIEHPFLNG-EVIRLDGA 256
DB 219 GQPAEYGAANVFLASEANFCTGIELLVYTGGA 249

RESULT 24
US-09-978-697-468
Sequence 468, Application us/09978697
Parent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: ASHKENAZI, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gierltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, Timothy A.
APPLICANT: Stewart, David L.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697

1	CURRENT FILING DATE: 2001-10-16
2	PRIOR APPLICATION NUMBER: 09/918585
3	PRIOR FILING DATE: 2001-07-30
4	PRIOR APPLICATION NUMBER: 60/063250
5	PRIOR FILING DATE: 1997-10-17
6	PRIOR APPLICATION NUMBER: 60/064249
7	PRIOR FILING DATE: 1997-11-03
8	PRIOR APPLICATION NUMBER: 60/065311
9	PRIOR FILING DATE: 1997-11-13
10	PRIOR APPLICATION NUMBER: 60/066364
11	PRIOR FILING DATE: 1997-11-21
12	PRIOR APPLICATION NUMBER: 60/077450
13	PRIOR FILING DATE: 1998-03-10
14	PRIOR APPLICATION NUMBER: 60/077632
15	PRIOR FILING DATE: 1998-03-11
16	PRIOR APPLICATION NUMBER: 60/077641
17	PRIOR FILING DATE: 1998-03-11
18	PRIOR APPLICATION NUMBER: 60/077649
19	PRIOR FILING DATE: 1998-03-11
20	PRIOR APPLICATION NUMBER: 60/077791
21	PRIOR FILING DATE: 1998-03-12
22	PRIOR APPLICATION NUMBER: 60/078004
23	PRIOR FILING DATE: 1998-03-13
24	PRIOR APPLICATION NUMBER: 60/078886
25	PRIOR FILING DATE: 1998-03-20
26	PRIOR APPLICATION NUMBER: 60/078936
27	PRIOR FILING DATE: 1998-03-20
28	PRIOR APPLICATION NUMBER: 60/078910
29	PRIOR FILING DATE: 1998-03-20
30	PRIOR APPLICATION NUMBER: 60/078939
31	PRIOR FILING DATE: 1998-03-20
32	PRIOR APPLICATION NUMBER: 60/079294
33	PRIOR FILING DATE: 1998-03-25
34	PRIOR APPLICATION NUMBER: 60/079556
35	PRIOR FILING DATE: 1998-03-26
36	PRIOR APPLICATION NUMBER: 60/079664
37	PRIOR FILING DATE: 1998-03-27
38	PRIOR APPLICATION NUMBER: 60/079689
39	PRIOR FILING DATE: 1998-03-27
40	PRIOR APPLICATION NUMBER: 60/079663
41	PRIOR FILING DATE: 1998-03-27
42	PRIOR APPLICATION NUMBER: 60/079728
43	PRIOR FILING DATE: 1998-03-27
44	PRIOR APPLICATION NUMBER: 60/079786
45	PRIOR FILING DATE: 1998-03-27
46	PRIOR APPLICATION NUMBER: 60/079920
47	PRIOR FILING DATE: 1998-03-30
48	PRIOR APPLICATION NUMBER: 60/079923
49	PRIOR FILING DATE: 1998-03-30
50	PRIOR APPLICATION NUMBER: 60/080105
51	PRIOR FILING DATE: 1998-03-31
52	PRIOR APPLICATION NUMBER: 60/080107
53	PRIOR FILING DATE: 1998-03-31
54	PRIOR APPLICATION NUMBER: 60/080165
55	PRIOR FILING DATE: 1998-03-31
56	PRIOR APPLICATION NUMBER: 60/080194
57	PRIOR FILING DATE: 1998-03-31
58	PRIOR APPLICATION NUMBER: 60/080327
59	PRIOR FILING DATE: 1998-04-01
60	PRIOR APPLICATION NUMBER: 60/080328
61	PRIOR FILING DATE: 1998-04-01
62	PRIOR APPLICATION NUMBER: 60/080333
63	PRIOR FILING DATE: 1998-04-01
64	PRIOR APPLICATION NUMBER: 60/080334
65	PRIOR FILING DATE: 1998-04-01
66	PRIOR APPLICATION NUMBER: 60/081070
67	PRIOR FILING DATE: 1998-04-08
68	PRIOR APPLICATION NUMBER: 60/081049
69	PRIOR FILING DATE: 1998-04-08
70	PRIOR APPLICATION NUMBER: 60/081071
71	PRIOR FILING DATE: 1998-04-08
72	PRIOR APPLICATION NUMBER: 60/081195
73	PRIOR FILING DATE: 1998-04-08

1	PRIOR APPLICATION NUMBER: 60/081203
2	PRIOR FILING DATE: 1998-04-09
3	PRIOR APPLICATION NUMBER: 60/081229
4	PRIOR FILING DATE: 1998-04-09
5	PRIOR APPLICATION NUMBER: 60/081955
6	PRIOR FILING DATE: 1998-04-15
7	PRIOR APPLICATION NUMBER: 60/081817
8	PRIOR FILING DATE: 1998-04-15
9	PRIOR APPLICATION NUMBER: 60/081819
10	PRIOR FILING DATE: 1998-04-15
11	PRIOR APPLICATION NUMBER: 60/081952
12	PRIOR FILING DATE: 1998-04-15
13	PRIOR APPLICATION NUMBER: 60/081838
14	PRIOR FILING DATE: 1998-04-15
15	PRIOR APPLICATION NUMBER: 60/082568
16	PRIOR FILING DATE: 1998-04-21
17	PRIOR APPLICATION NUMBER: 60/082569
18	PRIOR FILING DATE: 1998-04-21
19	PRIOR APPLICATION NUMBER: 60/082704
20	PRIOR FILING DATE: 1998-04-22
21	PRIOR APPLICATION NUMBER: 60/082804
22	PRIOR FILING DATE: 1998-04-22
23	PRIOR APPLICATION NUMBER: 60/082700
24	PRIOR FILING DATE: 1998-04-22
25	PRIOR APPLICATION NUMBER: 60/082797
26	PRIOR FILING DATE: 1998-04-22
27	PRIOR APPLICATION NUMBER: 60/082796
28	PRIOR FILING DATE: 1998-04-23
29	PRIOR APPLICATION NUMBER: 60/083336
30	PRIOR FILING DATE: 1998-04-27
31	PRIOR APPLICATION NUMBER: 60/083322
32	PRIOR FILING DATE: 1998-04-28
33	PRIOR APPLICATION NUMBER: 60/083392
34	PRIOR FILING DATE: 1998-04-29
35	PRIOR APPLICATION NUMBER: 60/083495
36	PRIOR FILING DATE: 1998-04-29
37	PRIOR APPLICATION NUMBER: 60/083496
38	PRIOR FILING DATE: 1998-04-29
39	PRIOR APPLICATION NUMBER: 60/083499
40	PRIOR FILING DATE: 1998-04-29
41	PRIOR APPLICATION NUMBER: 60/083545
42	PRIOR FILING DATE: 1998-04-29
43	PRIOR APPLICATION NUMBER: 60/083544
44	PRIOR FILING DATE: 1998-04-29
45	PRIOR APPLICATION NUMBER: 60/083542
46	PRIOR FILING DATE: 1998-04-29
47	PRIOR APPLICATION NUMBER: 60/083558
48	PRIOR FILING DATE: 1998-04-29
49	PRIOR APPLICATION NUMBER: 60/083559
50	PRIOR FILING DATE: 1998-04-29
51	PRIOR APPLICATION NUMBER: 60/083500
52	PRIOR FILING DATE: 1998-04-29
53	PRIOR APPLICATION NUMBER: 60/083742
54	PRIOR FILING DATE: 1998-04-30
55	PRIOR APPLICATION NUMBER: 60/084366
56	PRIOR FILING DATE: 1998-05-05
57	PRIOR APPLICATION NUMBER: 60/084414
58	PRIOR FILING DATE: 1998-05-06
59	PRIOR APPLICATION NUMBER: 60/084441
60	PRIOR FILING DATE: 1998-05-06
61	PRIOR APPLICATION NUMBER: 60/084637
62	PRIOR FILING DATE: 1998-05-07
63	PRIOR APPLICATION NUMBER: 60/084639
64	PRIOR FILING DATE: 1998-05-07
65	PRIOR APPLICATION NUMBER: 60/084640
66	PRIOR FILING DATE: 1998-05-07
67	PRIOR APPLICATION NUMBER: 60/084598
68	PRIOR FILING DATE: 1998-05-07
69	PRIOR APPLICATION NUMBER: 60/084600
70	PRIOR FILING DATE: 1998-5-07
71	PRIOR APPLICATION NUMBER: 60/084627
72	PRIOR FILING DATE: 1998-05-07
73	PRIOR APPLICATION NUMBER: 60/084643
74	PRIOR FILING DATE: 1998-05-07
75	PRIOR APPLICATION NUMBER: 60/085339

Thu Jun 26 06:55:08 2003

us-09-931-186-4.rapb

Page 14

PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 22.4%; Score 291.5; DB 9; Length 270;
Best Local Similarity 31.7%; Pred. No. 1,2e-18;
Matches 86; Conservative 42; Mismatches 106; Indels 37; Gaps 8;

QY 1 MAAVRSVKGLVAVITGASGLIATRELYGOGASVLLDPRNSGGEQAKKLNVCV 60
DB 1 MATGTR-YAGRVVVVTGGGRIAGIVRAFNAGARVYICDKDESGGRLAQEL-PCAVP 58
QY 61 APANVTSEKDVOTATLAKNGFRVDVAVNCAGIAVASKTYNKGOTHTLEDFORVLDV 120
DB 59 ILCCVLTGDDVKTIVSETIRFRGLDCCVNNAGHPP-----QRPETSAQGFROLEL 113
QY 121 NMGTEVIRLVAGEMGONEDDGGGQGVITNATSAVAFEGQYGAAYSAKSGIYKML 180
DB 114 NLCTVTLTKLALPYLAKSQ-----GNVINISLVLGAGQAVYVATKGAIVAMTK 166
QY 181 PIADLPIGIRVITAPGLFPTLTSPEKVCNPLASQVPP-----SRL 227
DB 167 ALADESPYGVYVNCISPGNTWPLME-----LAALMPDRATIRGMLAQPLGRM 218
QY 228 GDPAEY-AHLVQAIENPFLNG-EVIRLDGA 256
DB 219 GQPAEVGAAMVFLASEANFCIGIELVLTGGA 249

RESULT 25
US-09-978-192A-468
Sequence 468, Application US/09978192A
Patent No. US2002017553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Fliwaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC9
CURRENT FILING DATE: 2001-10-15
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334

Thu Jun 26 06:55:08 2003

us-09-931-186-4.rapb

Page 15

PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082565
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 22.4%; Score 291.5; DB 9; Length 270;
Best Local Similarity 31.7%; Pred. No. 1.2e-18;
Matches 86; Conservative 42; Mismatches 106; Indels 37; Gaps 8;

QY 1 MAAAVSYGCVAVITGASGGLATAERLYVGGSASAVLLDIPNSGGEQAOKKLGNNYF 60
DB 1 MATGTR-YAKGVVAVVGGGRGIGAGIVRAFNVSAGARVVICDDKDESGRLBEQL -PGAYF 58
QY 61 APADVTSEKDVOTALALAKGFRGVAVNACIAVASSTYNNKRGOTHTLEDFORVDV 120
DB 59 ILCDVTQEDDVKTIVSETIRFRGLDCVYNNAGHPP-----QREPEISAOQFROLLEL 113
QY 121 NMGTFVITLAVGEMQONFDDGGQRGVYINTASVAAFEGGVCAAYSASKGIYGMTL 180
DB 114 NLGTYTLTKLALPYLKSO-----GNVINTSLVGATGCAQAYPYATKCAVYAMK 166
QY 181 PIARDLAPIGIRVWTINPGLFTPLTSLPEKVCNFLASOVPP-----SRL 227
DB 167 ALALDESPYGVARNCSIGNWTPLWEE-----LAALMPDPRAITREGMIAOPLGRM 218
QY 228 GDPAET-AHLVQALTEPFLNG-EVIRLDDA 256
DB 219 GOPAEVGAARVFLASEANFCTGIELVLTGSA 249

Search completed: June 23, 2003, 14:59:45
Job time : 22.333 secs

```

RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azeredo V., Bertolo M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriis R., Bourcier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Ertlan K.D., Errington J., Fabret C., Ferrazi A., Fougere D.,
RA Fritsch C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.T., Glaser P., Goffeau A., Golightly E.T., Grandi G.,
RA Hilbert H., Guy B.J., Haga K., Hachez J., Harwood C.R., Henaux A.,
RA Hilbert H., Holstappel S., Hosono S., Hulio M.F., Ilaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogikawa A., Oudega B., Park S.H.,
RA Paro V., Pohl T.M., Portetlelle D., Portwille S., Prescott A.M.,
RA Prescan E., Pujic P., Purnelle B., Rapoport G., Ray M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter P., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosaio V., Uchiyama S., Vandendol M., Vanlier F., Vasseroiti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzeneiger T.,
RA Winters P., Wiput A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Darchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis";
RT Nature 390:249-256(1997)
RL
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X73124; CA51638.1;
DR EMBL: Z99123; CA51799.1;
DR PIR: S39737; S39737.
DR HSP: P50162; IAE1.
DR Subtilisin; B610628; ywFD.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PRO0080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT.1.
KW Hypothetical protein: Oxidoreductase: Complete proteome.
FT NP_BIND 11 33 NAD OR NADP (By SIMILARITY).
FT ACT_SITE 154 154 By SIMILARITY.
SQ
SEQUENCE 255 AA; 27324 MW; 20AA2259HFB889B CRC64;

Query Match 23.1%; Score 301; DB 1; Length 255;
Best Local Similarity 32.7%; Pred. No. 1.7e-16;
Matches 88; Conservative 42; Mismatches 93; Indels 46; Gaps 8;

```

```

OY 187 APGIRVMTAPGLFGLTLLSLPEKYCNFL-----ASQVPPPSRLGDAFY 233
DB 173 AKHGRNVCOPGIIIDP-----LNEK--SEFENNEGTLEIKERKAKVNDLLRLGKPEEI 226
OY 234 AHLVQAITE--NPLNGEVIRLDAIMQ 260
DB 227 ANVMLFLASDLSSYMTGSATATADGGYTAQ 255

RESULT 16
2BHD_STREX
ID 2BHD_STREX STANDARD: PRT: 255 AA.
AC P19992;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE 20-beta-hydroxysteroid dehydrogenase (EC 1.1.1.53).
OS Streptomyces exfoliatus (Streptomyces hydrogans).
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI-TaxID=1905;
RN [1]
RP SEQUENCE.
RA MEDLINE=90306362; PubMed=2194840;
RA Marekov L., Krook M., Joernvall H.;
RT "Prokaryotic 20 beta-hydroxysteroid dehydrogenase is an enzyme of the
RT 'short-chain, non-metalloenzyme' alcohol dehydrogenase type.";
RL FEBS Lett. 266:51-54(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=92052211; PubMed=1946424;
RA Ghosh D., Weeks C.M., Grochulski P., Duax W.L., Erman M.,
RA Rimsay R.L., Orr J.C.;
RT "Three-dimensional structure of holo 3 alpha,20 beta-hydroxysteroid
RT dehydrogenase: a member of a short-chain dehydrogenase family.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10064-10068(1991).
CC -1- CATALYTIC ACTIVITY: Androstan-3-alpha,17-beta-diol + NAD(+) = 17-
CC beta-hydroxyandrostane-3-one + NADH.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDS) FAMILY.
CC PIR: S10707; S10707.
DR PDB: 1HSD; 31-AUG-94.
DR PDB: 1HDC; 07-FEB-95.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PRO0080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT.1.
KW Oxidoreductase; NAD; Steroid metabolism; 3D-structure.
FT NP_BIND 10 34 NAD (By SIMILARITY).
FT ACT_SITE 152 152
FT ACT_SITE 152 152
SQ
SEQUENCE 255 AA; 26484 MW; 9CB93CB66A628D5 CRC64;

Query Match 23.0%; Score 300; DB 1; Length 255;
Best Local Similarity 33.2%; Pred. No. 2.1e-16;
Matches 85; Conservative 48; Mismatches 103; Indels 20; Gaps 8;

```

QY 242 E--NPFNGEVIKLDG 255
 DB 226 SDTSYVNGAEIADVG 241

RESULT 17
 YAVI_RHISN STANDARD: PRT: 548 AA.

AC 053217;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Putative short-chain type dehydrogenase/reductase YAVI (EC 1.1.1.159).
 GN YAVI.
 OS Rhizobium sp. (strain NGR234).
 OG Plasmid sym pNGR234.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=394;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-97305956; PubMed-9163424;
 RA Freiderg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
 RA Perret X.;
 RT "Molecular basis of symbiosis between Rhizobium and legumes."; a
 RL Nature 387:394-401(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96389014; PubMed-8796346;
 RA Freiderg C., Perret X., Broughton W.J., Rosenthal A.;
 RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
 RT NGR234 using dye terminators and a thermostable 'sequenase': a
 RT beginning";
 RL Genome Res. 6:590-600(1996).
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY. CONTAINS TWO DOMAINS.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

DR EMBL: Z68203; CA92424.1; ALT_INIT.
 DR EMBL: AE000101; AAB91897.1; -.
 DR HSSP: P50163; ZAE1.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 2.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
 KW Multifunctional enzyme.
 KM DOMAIN 1 250
 FT DOMAIN 1 250
 FT NP_BIND 12 548
 FT NP_BIND 12 37
 FT ACT_SITE 154 154
 FT NP_BIND 280 304
 FT ACT_SITE 420 420
 FT SEQUENCE 548 AA; 57593 MW; 399598C5DF17C23F CRC64;
 SQ

Query Match 22.6%; Score 294.5; DB 1; Length 548;
 Best Local Similarity 33.6%; Pred. No. 1.3e-15;
 Matches 86; Conservative 41; Mismatches 100; Indels 29; Gaps 8;

QY 10 GIVAVITGGAGSGIGTAERTVGGASAVILDPNNGGGEAKKGNVCFAPADYTSK 69
 DB 9 GRIIVITGAGGIGRALVDLFFAANGDVYVADLPDSGVIELGNLDEPHIGLEVDSRED 68

QY 70 DVQATALAKGKRGFVAVNACGI---AVASKTYNLKKGQTHLEDFQVRLVDVLMGT 125
 DB 69 DVVALRALLEKRRSRILEVLNMMNGIGPTMAATADT-----ALEDFQALAIIVLGA 119

QY 126 FNVIRLVAGEMGNEPDGQGRGVIIINTASVAFEGOVGAAYASAKSGIYGTLPARD 185
 DB 120 YSVACETAKLM---KPG-----AAIVNWSLGLLGNPKRSAYASAKGILISTTKSLACR 171

QY 186 LAPIGIRVMTIAPGLFTPLTSLPERV---CNFLASGVFPFSLGDPAEYAHLYO--A 239
 DB 172 MASRGIVRTAVAPGHVATPVAVEL-ERAGKLDVSAIRRVPL-GRIARDDEIARAVRFLA 229

QY 240 ITEMPFNGEVIKLDG 255
 DB 230 SAQASYTTGGTLLVVDG 245

RESULT 18
 BA7L_EUBSP STANDARD: PRT: 249 AA.

AC P07914;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 7-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159) (Bile acid
 DE 7-dehydroxylase) (7-alpha-HSDH) (Bile acid-inducible protein).
 GN BA7L AND BA7A3.
 OS Eubacterium sp. (strain VPI 12708).
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=29347;
 RN [1]
 RP SEQUENCE FROM N.A. (BA7A3).
 RX MEDLINE-90330548; PubMed-2376563;
 RA Gopal-Srivastava R., Mallonee D.H., White W.B., Hylemon P.B.;
 RT "Multiple copies of a bile acid-inducible gene in Eubacterium sp.
 RT strain VPI 12708.";
 RL J. Bacteriol. 172:4420-4426(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (BA7A1).
 RX MEDLINE-86197993; PubMed-2834320;
 RA Coleman J.P., White W.B., Lilewski M., Hylemon P.B.;
 RT "Nucleotide sequence and regulation of a gene involved in bile acid
 RT 7-dehydroxylation by Eubacterium sp. strain VPI 12708.";
 RL J. Bacteriol. 170:2070-2077(1988).
 RN [3]
 RP SEQUENCE OF 1-55 FROM N.A. (BA7A1), AND SEQUENCE OF 1-33.
 RX MEDLINE-87165759; PubMed-3549693;
 RA Coleman J.P., White W.B., Hylemon P.B.;
 RT "Molecular cloning of bile acid 7-dehydroxylase from Eubacterium sp.
 RT strain VPI 12708.";
 RL J. Bacteriol. 169:1516-1521(1987).
 CC -1 FUNCTION: 7-ALPHA-DEHYDROXYLATION OF CHOLIC ACID, YIELDING
 CC DEOXYCHOLIC ACID AND LITHOCHOLIC ACID, RESPECTIVELY. HIGHEST
 CC AFFINITY WITH TAUROCHENODEOXYCHOLIC ACID.
 CC CATALYTIC ACTIVITY: 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-
 CC cholanate + NAD(+) = 3-alpha,12-alpha-dihydroxy-7-oxo-5-beta-
 CC cholanate + NADH.
 CC -1 PATHWAY: Bile acid catabolism.
 CC -1 INDUCTION: PRESENCE OF C(24) BILE ACIDS CONTAINING A
 CC 7-ALPHA-HYDROXY GROUP.
 CC -1 SIMILARITY: THERE ARE THREE GENES FOR BA7A PROTEINS: BA7A1 IS
 CC IDENTICAL TO BA7A3 AND THERE IS 81% IDENTITY WITH BA7A2.
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

DR EMBL: M34658; AAB61155.1; -.
 DR EMBL: M19654; AAB61154.1; -.
 DR EMBL: M15813; AAB61153.1; -.

	RESULT	19
FABG_VIBHA		
ID	FABG_VIBHA	STANDARD; PRT; 244 AA.
AC	P55336;	
DT	01-OCT-1996 (Rel. 34, Created)	
DT	01-OCT-1996 (Rel. 34, Last sequence update)	
DT	01-OCT-1996 (Rel. 34, Last annotation update)	
DE	3-oxoacyl-[acyl-carrier protein] reductase (Ec 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).	
GN	FABG.	
OS	Vibrio harveyi.	
OC	Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.	
OX	NCBI_Taxid=669;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=B392;	
RX	MEDLINE=9613497; PubMed=8550484;	
RA	Shen Z., Byers D.M.;	
RT	"Isolation of vibrio harveyi acyl carrier protein and the fabg, accp,	
RL	J. Bacteriol. 178:571-573(1996)."	
CC	-1 CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +	
CC	NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADH.	
CC	-1 PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS	
CC	PATHWAY:	
CC	-1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDOXTASES	
CC	(SDR) FAMILY.	
CC		
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	

```

CC CC RESULT 20
AC FABG_AQUAE STANDARD; PRT: 248 AA.
AC 067610;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
DE FABG OR AC_1716.
OS Agulfex aeolicus.
OC Bacteria; Aquificae; Aquificaceae; Aquificales; Aquificaceae;
OX Agulfex.
OX NCBI_TaxId=63363;
[ ]
RP SEQUENCE FROM N.A.
RP STRAIN-VES.
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., R.
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aulsebrook M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Agulfex
RT aeolicus."
RL Nature 397:353-358(1998).
CC -1- CATALYTIC ACTIVITY: (3r)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

```

CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AE000752; AAC07575.1; -
 DR HSSP: P50163; 2AE1.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT ACCT_SITE 12 NADP (BY SIMILARITY).
 FT ACCT_SITE 157 157
 SQ SEQUENCE 248 AA; 26867 MW; 5CFD9EB9AD832C5 CRC64;
 Query Match 22.3%; Score 290.5; DB 1; Length 248;
 Best Local Similarity 30.0%; Pred. No. 1,1e-15;
 Matches 77; Conservative 50; Mismatches 109; Indels 21; Gaps 6;
 QY 8 VKGLVAVITGASGLGLATAEERLVGQASAVLLDLPNSGGEAARKIGN---NCVFAPA 63
 DB 5 LQGVSLVSTGRGIGRAIAEKLASGSTVITGTSGERAKVAEIAIKYGVAKHGVEM 64
 QY 64 DVTSEVDVGTALALAKGKRGVDVAVNCAGIYASKTYNLKKGTHLEDPORVLDVLM 123
 DB 65 NLISESINKAFEEIYNLVDSIDILVNNAGITRDKLFLRM-----SLIDMEVLKVNLT 118
 QY 124 GFENVIRLVAGENGQNEPDQSGQR-GVILINPASAFAEGVQQAAYSAKSGIVMTLPI 182
 DB 119 GFELVTVNGSLRKMKIR-----QRMGRIVNISSVYGFNGVNVSTKAGLIGFTKSL 171
 QY 183 ARDLAIGIRVMTIAGLEGTPLTSLPKVNCNPLASQVFPFSLGDPREAHLYQATIE 242
 DB 172 AKELARNVLVANVAAAGFETDMTAVLSEIKQYKKEQLPL-GRGSPPEVANVVLFCOS 230
 QY 243 N--PFLNGEYIRLDGAI 257
 DB 231 ELASVITGEVYHNGSM 247
 RESULT 21
 FABG_ECOLI STANDARD; PRT; 244 AA.
 AC P25716; P78221;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
 GN acyl carrier protein reductase).
 DE FABG OR B1093.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia
 OX NCBI-TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=92210530; Pubmed=1556094;
 RA Rawlings M., Cronan J.E. Jr.;
 RT "The gene encoding Escherichia coli acyl carrier protein lies within
 RT a cluster of fatty acid biosynthetic genes".
 RL J. Biol. Chem. 267:5751-5754(1992).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=K12 / MG1655;
 RC MEDLINE=97426617; Pubmed=9278503;
 RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Colado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12".
 RL Science 277:1453-1474(1997).

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97061202; Pubmed=8905232;
 RA Oshima T., Alba H., Baba T., Fujita K., Hayaishi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kasimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiuchi T.;
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-153(1996).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M84991; AA23739.1; -
 CC EMBL: AE000210; AAC74177.1; -
 CC EMBL: D90745; BAA35901.1; -
 CC PIR: B42147; B42147.
 DR HSSP: P29132; 1DE1.
 DR Ecocore: E011318; fabG.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 10 34 NADP (BY SIMILARITY).
 FT ACCT_SITE 151 151
 FT CONFLICT 30 30 A->G (IN REF. 1).
 FT SEQUENCE 244 AA; 25560 MW; 48BC1P2A7F7EFPD9 CRC64;
 Query Match 22.2%; Score 289.5; DB 1; Length 244;
 Best Local Similarity 30.0%; Pred. No. 1,3e-15;
 Matches 76; Conservative 50; Mismatches 112; Indels 15; Gaps 4;
 QY 9 KGVLAVITGASGLGLATAEERLVGQASAVLLDLPNSGGEAARKIGNCVFAPADYTS 68
 DB 4 ECKTALVYGASRGIGRAIAEKLASGSTVITGTSGERAKVAEIAIKYGVAKHGVEM 63
 QY 69 KDVTALALAKGKRGVDVAVNCAGIYASKTYNLKKGTHLEDPORVLDVLMGFENV 128
 DB 129 IRLVAGENGQNEPDQSGQRVYINPASAFAEGVQQAAYSAKSGIVMTLPIARDAP 188
 QY 118 SRAVRAAMRK-----THGRITITGSVVGTMNGGQANVYAAAGLIGFSKSLAREVNS 171
 DB 64 ASIESVLKIRAEFEVDILVNNAGITRDNILMRKO-----EEMNDIITNLSVEFL 117
 QY 129 IRLVAGENGQNEPDQSGQRVYINPASAFAEGVQQAAYSAKSGIVMTLPIARDAP 188
 DB 189 IIRVMTIAGLEGTPLTSLPEKVCNPLASQVFPFSLGDPREAHLYQ-ATLENPFL 246
 DB 172 KRIYVNVAPGFIEDMTRALSDQRAIGLQV-AGRLGGAQELANVAVLASDEAAVYI 230
 QY 247 NGEVIRLDGAI 259
 DB 231 TGETLVHNGSM 243
 RESULT 22
 UCPLA_SALT
 ID UCPLA_SALT
 AC P37441; STANDARD; PRT; 263 AA.

DT 01-OCT-1994 (Rel. 30, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Oxidoreductase ucpa (EC 1.-.-.-).
 GN UCPC OR STM2445 OR STY2682.
 OS Salmonella typhimurium, and
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 ON NCBI_TaxId=602, 601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 LT2.";
 RN Nature 413:852-856(2001).
 RL [2]
 RP SEQUENCE OF 204-263 FROM N.A.
 RC SPECIES=S.typhimurium;
 RX MEDLINE=91358382; PubMed=1909324;
 RA Hryniewicz M.M., Kredich N.M.;
 RT "The cyst promoter of *Salmonella typhimurium*: characterization of two
 RT binding sites for CysB protein, studies of in vivo transcription
 RT initiation, and demonstration of the anti-inducer effects of
 RT thiosulfate.";
 RL J. Bacteriol. 173:5876-5886(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhi; STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebalha M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Feltwell A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Fournier T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jorgels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AE008810; AL21339.1; -
 DR EMBL: AL627274; CAD07676.1; -
 DR PIR: A38121; A38121.
 DR StyGene; SG10424; ucpa.
 DR InterPro: IPR002198; ADH_short.
 DR PROSITE: PS00061; ADH_SHORT; FALSE_NEG.
 KM Oxidoreductase; Complete proteome.
 FT CONFLICT 218 L-> M (IN REF. 2).
 FT CONFLICT 258 S-> T (IN REF. 2).
 FT CONFLICT 263 V-> I (IN REF. 2).
 FT SEQUENCE 263 AA; 27870 MM; 81H26CAD9BD4534E CRC64;
 SQ
 Query Match 22.1%; Score 288; DB 1; Length 263;
 Best Local Similarity 32.2%; Pred. No. 1.8e-15;
 Matches 85; Conservative 38; Mismatches 105; Indels 36; Gaps 8;

QY 10 GLVAVITGASGLGATAEKLVGOGASAVLLDPNSGGEAOKL-----GNQVEAP 62
 DB 6 GKTLITIGASGIEGIAFRFARGANILLIDISD-----ETKLADELGRGRHCAVX 60
 QY 63 ADVTSEKDVOTALALAKGEGVAVNACGIAVASTYLNKKGOTHTLDFORVLDVNT 122
 DB 61 ADVADPASVQAARVARKETESRIDILVNNAGVCLGNFLDKSE-----EDRDFHIDINI 114
 QY 123 MGTENVIRLVAGEKQNEPDGQGVYINTASTAA-FEGVGAASASGKGVKGLP 181
 DB 115 KGVNWTAKVLPENIKRSD-----GRIVMSSVTGDMVADPGTAVALSKAAIVGLTKS 168
 QY 182 IARDLAPIGIRVMTIAPGLFGTPLTSL-----PEKCNFLASQVPPSRIDPAEY 233
 DB 169 LAVERASGIRVNAICPQYVTPMAESIAKSNPDDESVLTEMAKAIPL-RLADPLEV 227
 QY 234 AHLVQ-AIENPFLNGEVRIDG 255
 DB 228 GELAAFLASDESSYLTGTQNVIDG 251
 RESULT 23
 PHBB_ALCEU STANDARD; PRT; 246 AA.
 ID PHBB_ALCEU
 AC P14697;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetoacetyl-CoA reductase (EC 1.1.1.36).
 GN PHBB.
 OS Alcaligenes eutrophus (Ralstonia eutropha).
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 ON NCBI_TaxId=510;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H16 / DSM 428 / ATCC 17699;
 RX MEDLINE=89359356; PubMed=2670935;
 RA Peoples O.P., Sinskey A.C.;
 RT "Poly-beta-hydroxybutyrate biosynthesis in *Alcaligenes eutrophus* H16.
 RT Characterization of the genes encoding beta-ketothiolase and
 RT acetoacetyl-CoA reductase.";
 RL J. Biol. Chem. 264:15293-15297(1989).
 CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxyacyl-CoA + NADP(+) = 3-oxoacyl-CoA + NADPH.
 CC -1- PATHWAY: Poly-beta-hydroxybutyrate biosynthesis; second step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: J04987; AAA21973.1; -
 DR PIR: B34340; KDALAE.
 DR HSSP: O70351; 1B3S.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KM Oxidoreductase; NADP; PHB biosynthesis.
 FT NP_BIND 8 NADP (BY SIMILARITY).
 FT ACT_SITE 153 BY SIMILARITY.
 FT SEQUENCE 246 AA; 26370 MM; AD6739ED0F5C93C06 CRC64;
 SQ
 Query Match 22.0%; Score 287.5; DB 1; Length 246;
 Best Local Similarity 31.9%; Pred. No. 1.8e-15;

[illegible][illegible]

```

RESULT 24
PHAB_ACISIP STANDARD; PRT; 248 AA.
ID PHAB_ACISIP
AC P50203;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Acetoacetyl-CoA reductase (EC 1.1.1.35).
GN PHAB.
OS Acinetobacter sp. (strain RA3849).
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=472;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95362679; PubMed=7638932;
RA Schumbi M.A., Bayly R.C., Davies J.K.;
RT "Phosphate concentration regulates transcription of the Acinetobacter
RT polyhydroxyalkanoic acid biosynthetic genes.";
RL J. Bacteriol. 177:4501-4507(1995).
CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxyacyl-CoA + NADP(+) = 3-oxoacyl-
CC CoA + NADPH.
CC -1- PATHWAY: Polyhydroxyalkanoic acid biosynthesis; second step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDS) FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb.slb.ch/announce/
CC or send an email to license@isb.slb.ch).
CC -----
CC DR EMBL: L37761; AAA99472.1; -.
CC DR HSSP: P19992; IHDC.
CC DR InterPro: IPR002198; ADH_short.
CC DR Pfam: PF00106; adh_short; 1.
CC DR PRINTS: PRO00080; SDRPAMITY.
CC DR PROSITE: PS00061; ADH_SHORT; 1.
CC DR Oxidoreductase; NADP.
CC FT AC_BIND 9 33 NADP (BY SIMILARITY).
CC FT AC_SITE 155 155 BY SIMILARITY.
CC FT NTSITE 248 AA; 26727 MW; 850E0DC659795123 CRC64;
CC SQ

```

```

RESULT 25
Y019_THEMEA STANDARD; PRT; 256 AA.
ID Y019_THEMEA
AC Q06316
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative oxidoreductase TM0019 (EC 1.-.-.-).
GN TM0019.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales;
OC Thermotogaceae; Thermotoga.
CX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RC MEDLINE=96125254; PubMed=8550425;
RA Kleczin A., Adams M.;
RT "Molecular and phylogenetic characterization of pyruvate and 2-
RT ketolysate ferredoxin oxidoreductases from Pyrococcus furiosus
RT and pyruvate ferredoxin oxidoreductase from Thermotoga maritima.";
RL J. Bacteriol. 178:248-257(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RC MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
RA Haft D.H., Hickey E.R., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher C.D., Garrett M.M.,
RA Stewart A.W., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heideberg J., Sutton G.G., Fleischmann R.P., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
CC - SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDS) FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X85171; CAA59459.1; -
DR EMBL: AE001690; AAD35113.1; -
DR HSSP: 070351; 1E6W.
DR TIGR: TM0019; -
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR

```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OK protein - protein search, using sw model

Run on: June 23, 2003, 14:23:47 ; Search time 15.6667 Seconds

(without alignments)
1601.559 Million cell updates/sec

Title: US-09-931-186-4

Perfect score: 1304
Sequence: 1 MAAAVRSVKGLVAVITGGAS.....ENPFLNGEYIRLDGAIKMPD 261

Scoring table:

BLASTX62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613442 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

PIR_73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	750	57.5	258	2 T20484	hypothetical prote
2	720	55.2	255	2 H83326	probable short-cha
3	711	54.5	255	2 AG3611	3-oxoacyl-(acyl-ca
4	671.5	51.5	250	2 A70554	probable dehydroge
5	670	51.4	255	2 H95360	probable imported
6	642	49.2	257	2 F97531	probable short-cha
7	642	49.2	257	2 AG2750	3-hydroxyacyl-CoA
8	595	45.6	260	2 C87264	3-oxoacyl-(acyl-ca
9	383.5	29.4	247	2 E70740	probable fabG2 pro
10	355	27.2	252	2 F83098	probable short-cha
11	343.5	26.3	249	2 F97338	3-ketoacyl-acyl ca
12	341	26.2	246	2 H72219	3-oxoacyl-(acyl ca
13	336.5	25.8	297	2 T51084	3-oxoacyl-(acyl-ca
14	334	25.6	320	2 S22450	3-oxoacyl-(acyl-ca
15	333.5	25.6	246	2 C83961	3-oxoacyl-(acyl-ca
16	333.5	25.6	251	2 AH2042	3-oxoacyl-(acyl-ca
17	332	25.5	246	2 H84136	3-oxoacyl-(acyl-ca
18	328.5	25.2	248	2 F83128	3-oxoacyl-(acyl-ca
19	326.5	25.0	243	2 E97919	3-oxoacyl-(acyl-ca
20	325.5	25.0	243	2 G95048	3-oxoacyl-(acyl-ca
21	324.5	24.9	243	2 G95048	3-oxoacyl-(acyl-ca
22	317	24.3	299	2 D90481	hypothetical prote
23	315.5	24.2	260	1 A48134	hypothetical prote
24	315.5	24.2	260	1 T36846	short-chain alcoh
25	315	24.2	267	2 T11579	probable dehydroge
26	314.5	24.1	259	2 H98137	probable short cha
27	314.5	24.1	259	2 H98137	3-oxoacyl-(acyl-ca
28	313.5	24.0	240	2 H75014	3-oxoacyl-(acyl-ca
29	313.5	24.0	247	2 S77280	3-oxoacyl-(acyl-ca

30	312.5	24.0	296	2 E87260	hypothetical prote
31	311	23.8	247	2 F82776	3-oxoacyl-(ACP) re
32	311	23.8	262	2 AB3545	toluenesulfonate z
33	309.5	23.7	244	2 AB0195	3-oxoacyl-(acyl-ca
34	309.5	23.7	246	2 A69621	3-oxoacyl-(acyl-ca
35	309	23.7	249	2 AG3121	dehydrogenase Atu4
36	309	23.7	253	2 H98165	3-oxoacyl-(acyl-ca
37	306	23.5	256	2 A10406	probable dehydroge
38	305	23.4	260	2 H70758	probable fabG3 pro
39	303.5	23.3	247	2 AG1300	3-ketoacyl-acyl ca
40	303	23.2	248	2 H98258	3-oxoacyl-(acyl-ca
41	303	23.2	248	2 A13025	3-oxoacyl-(acyl-ca
42	301.5	23.1	247	2 AG1672	3-ketoacyl-acyl ca
43	301	23.1	245	2 AE3517	glucose 1-dehydrog
44	300.5	23.0	255	1 S39377	hypothetical prote
45	300	23.0	256	2 T26723	hypothetical prote
46	300	23.0	255	1 S47054	probable dehydroge
47	298	22.9	252	1 S10707	20beta-hydroxyster
48	296.5	22.7	252	2 B90495	hypothetical prote
49	296	22.7	258	2 C70885	probable dehydroge
50	294	22.5	245	2 AE3517	3-oxoacyl-(acyl-ca
51	294	22.5	255	2 H84288	3-oxoacyl-(acyl-ca
52	293	22.5	249	1 T36596	probable short cha
53	291.5	22.4	249	1 B37762	bile acid 7-dehydr
54	291	22.3	248	2 T12051	3-oxoacyl-(acyl-ca
55	290.5	22.3	258	2 D95284	probable imported
56	290	22.2	248	2 H70447	3-oxoacyl-(acyl-ca
57	289.5	22.2	272	2 AG3359	glucose 1-dehydrog
58	288	22.1	244	1 B42147	3-oxoacyl-(acyl-ca
59	287.5	22.0	253	2 AB0812	probable oxidoredu
60	287.5	22.0	246	1 RDALAE	acetoacetyl-CoA re
61	286.5	22.0	303	2 T46064	short-chain alcoh
62	286.5	22.0	244	2 G90812	3-oxoacyl-(acyl-ca
63	286.5	22.0	244	2 C85672	3-oxoacyl-(acyl-ca
64	285.5	21.9	254	2 G75333	3-oxoacyl-acyl car
65	284.5	21.8	255	2 G82644	2,5-dichloro-2,5-c
66	284.5	21.8	256	2 E72427	oxidoreductase, sh
67	283.5	21.7	257	2 A72395	oxidoreductase, sh
68	283.5	21.7	244	2 AD0642	3-oxoacyl-(acyl-ca
69	283.5	21.7	253	2 B86737	acetoin dehydrogen
70	282.5	21.6	272	2 A99950	hypothetical prote
71	282	21.6	251	2 C87474	hypothetical prote
72	281.5	21.6	255	2 D72377	oxidoreductase, sh
73	279.5	21.4	241	1 DEK98	acetoacetyl-CoA re
74	279.5	21.4	248	1 S06998	acetoacetyl-CoA re
75	279	21.4	240	2 E81695	3-oxoacyl-(acyl ca
76	279	21.4	258	2 F87312	acetoacetyl-CoA re
77	278	21.3	262	2 B97588	acetoind(diacetyl)r
78	278	21.3	262	2 AG2809	short chain dehydr
79	277.5	21.3	289	2 D69825	glucose 1-dehydrog
80	277	21.2	260	2 F82954	probable short-cha
81	276	21.2	249	1 A31841	bile acid dehydrox
82	276	21.2	285	1 A65017	probable 3-oxoacyl
83	276	21.2	285	2 A91041	probable oxidoredu
84	276	21.2	319	2 D85885	probable oxidoredu
85	276	21.2	319	2 S22416	3-oxoacyl-(acyl-ca
86	275.5	21.1	248	2 T44361	acetoacetyl-CoA re
87	275	21.1	246	1 S29379	acetoacetyl-CoA re
88	275	21.1	267	2 B87578	hypothetical prote
89	274.5	20.9	248	2 B97223	probable 3-ketacy
90	272.5	20.9	244	2 T44434	3-oxoacyl-(acyl-ca
91	272.5	20.9	286	2 G83378	probable short-cha
92	272	20.9	251	2 G72389	oxidoreductase, sh
93	272	20.9	259	2 E95903	probable dehydroge
94	272	20.9	263	2 S01227	glucose 1-dehydrog
95	270.5	20.7	240	2 F75021	3-ketoacyl-acyl ca
96	270.5	20.7	248	2 F71558	probable oxoacyl (
97	270.5	20.7	262	2 D97325	3-oxoacyl-acyl car
98	270.5	20.7	268	2 A86378	protein F2109.2 [1
99	270	20.7	308	2 G96016	probable gluconat
100	269.5	20.7	246	2 B89896	3-oxoacyl-(acyl-ca

Db 238 NDYMNGEVIRLDGAIRMQP 256

RESULT 7
AG2750
3-hydroxyacyl-CoA dehydrogenase type II Atut1415 [imported] - Agrobacterium tumefaciens
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C:Accession: AG2750
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayarin, T.; Levy, R.; Li, M.; McCell
r, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AG2750
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1257 <KUR>
A:Cross-references: GB:HE008688; PDB:1AI4241.1; PID:9177339833; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atut1415
A:Map position: circular chromosome
A:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

	Query Match	45.6%	Score 595;	DB 2;	Length 260;
	Best Local Similarity	51.0%;	Pred. No. 2,38-39;		
	Matches 130;	Conservative 30;	Mismatches 89;	Indels 6;	Gaps 2
QY	11	LVAVTTGGGASGIGLTAERLYGQGSANVLDLPMSGGEAOAKKLGNVCYFAPADVYSESD	70		
DB	7	VAAVVTGGGSGSGEATATAPALAAQGVKALFEMNEERELQYAKKEIGG--VFCKRYVNTSDD	64		
QY	71	VQFALALARKGKRGPDVAVVNCAGLAVASKTYNKKQGTHT---LEDPFVLDVNLMGTF	126		
DB	65	VDAGFEKRAARAAGQERILLYNCACGTGNMAKTSRDKAIGETKHFFLPDAFDRIITNLNVGFF	124		
QY	127	NVRLVYAGMGONPEDDGGQKGVLIINTASVAEFGQYGAAYSASKSGGIYGMTLPIARL	186		
DB	125	RCIAKSAKAMLDLEPLEDGERGAYVNTASVAEFGQGAAYSASKGGVGMTLPIARL	184		
QY	187	APIGIRVMTIADGLFTPLTSLPEKYCNFLPASQVPPSLGDPAPAEAYHLVQAILIENPL	246		
DB	185	MGEGRIVNTIILPGIFINTPLMNNAPAEAYKAGLAASVPEPKRLGHPDEEYQAALMTMGCVF	244		
QY	247	NGEVIITLDGAIRMP	261		
DB	245	NGEDVRLDGGIRMAP	259		

N:Alternate names: protein B2A19.180
 C:Species: Neurospora crassa
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 24-May-2001
 C:Accession: T51084
 R:Schulze, U.; Aisen, V.; Hohnsbeil, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000
 A:Reference number: 225286
 A:Accession: T51084
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-297 <SCD>
 A:Cross-references: EMBL:AL390092; GSPDB:GN00116; NCSP:B2A19.180
 A:Experimental source: EAC clone B2A19; strain OR74A
 C:Genetics:
 A:Gene: NCSP:B2A19.180
 A:Map position: 6
 A:Introns: 218/1; 249/1
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.8%; Score 336.5; DB 2; Length 297;
 Best Local Similarity 31.6%; Pred. No. 4.9e-19;
 Matches 97; Conservative 40; Mismatches 103; Indels 67; Gaps 8;

QY 5 VRSYKGLAVITGGASGLIATAEELVGGASAVLDDLPNS-----GGEA 49
 DB 1 MRLSLHQAALITGGSGIGLAIRRLYLEGCVTLTGRTSTLQASQSLLSQPLHSPA 60
 QY 50 CAKRLGNVCVAPADYSEKDVQAL-ALAKGRGRVAVNCAGINVAS---KTYLKK 105
 DB 61 QPSPDKRVSTHPLNVTSSASSWEDLLOSNSKGRKVDILINCAGITQPSLMKT----- 115
 QY 106 GQHTLEDFQVFLDVNLGTFNVIRLVAGENGQNEP-----DOGG----- 145
 DB 116 ---SIEVEGLDPTNLKGLTYLGCKFVGRAFLNRPSQHPHRYKADGAGAGVEGTEE 171
 QY 146 -----QREVINTASVAFAEGVQQAAYSAKSGIVKTLPIADLAPIG 190
 DB 172 KGEKGQGVGEVQVERGVIIIVASLAKQKGVITSTVYAAKAGVGLTSLAHEGRSG 231
 QY 191 IRVMTIAPGLFGTPLLTLSPKVCNFTLASQVPPFSRLDDPAEYHLYVQAITENPFLNGEV 250
 DB 232 IRVNAVLPGLYETDWTITLKNP---SILQQLPL-GRGTTDEVADALFLIKNPYANNVCV 287
 QY 251 IRLDGAI 257
 DB 288 LNLDSGL 294

RESULT 14
 S22450
 3-oxoacyl-(acyl-carrier-protein) reductase (EC 1.1.1.100) precursor, NADPH-dependent [va
 N:Alternate names: beta-ketoacyl-ACP reductase
 C:Species: Cuphea lanceolata
 C:Date: 16-Feb-1995 #sequence_revision 23-Feb-1996 #text_change 17-Mar-2000
 C:Accession: S22450; S19832
 R:Klein, B.; Pavlovski, K.; Hoerlicke-Grandpierre, C.; Schell, J.; Toepfer, R.
 Moli. Gen. Genet. 233, 122-128, 1992
 A:Title: Isolation and characterization of a cDNA from Cuphea lanceolata encoding a beta
 A:Reference number: S22450; MIMD:92293104; PMID:1376402
 A:Accession: S22450
 A:Molecule type: mRNA
 A:Residues: 1-320 <KLE>
 A:Cross-references: EMBL:X64566; NID:q18045; PIDN:CAA45866.1; PID:q18046
 A:Experimental source: immature embryo
 C:Genetics:
 A:Gene: Ckr27
 A:Gene: nuclear
 A:Function:
 A:Description: EC 1.1.1.100 [validated, MIMD:92293104]
 A:Pathway: fatty acid biosynthesis
 A:Note: Integral part of the fatty acid synthase type II
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 C:Keywords: chloroplast; fatty acid biosynthesis; NADP; oxidoreductase

F:1-63/Domain: transit peptide (chloroplast) #status predicted <NP>
 F:64-320/Product: 3-oxoacyl-(acyl-carrier-protein) reductase #status predicted <NP>
 F:78-258/Domain: short-chain alcohol dehydrogenase homology <SMDH>
 F:227/Active site: Tyr #status predicted

Query Match 25.6%; Score 334; DB 2; Length 320;
 Best Local Similarity 32.7%; Pred. No. 8.4e-19;
 Matches 87; Conservative 46; Mismatches 111; Indels 22; Gaps 6;

QY 2 AAARSRKGLAVITGGASGLIATAEELVGGASAVLDDLPNSGGEA-----QAKRLGN 56
 DB 69 AGAGGVSESPVYIVTASGIGKALISL-GRAGCVLVNVRSSKEAEVSEKELEAFEG 127
 QY 57 NCYFAPADYSEKDVQALALAKKGRGRVAVNCAGINVASKITKKGQHTLEDQR 116
 DB 128 QALTFGVDVSEKEDVAMKRTAVDAGVTDLVNNAGITRDGLMKRKSQ-----WQE 181
 QY 117 VLDVNLGTFNVIRLVAGENGQNEPDQGRVYINTASVAFAEGVQQAAYSAKSGIV 176
 DB 182 VIDNLNLTGVELCTQAANKIMMK-----KKGRILIASVGLVGNAGANYSAAKAGVI 235
 QY 177 GMTLPIARDLAPICIRVMTIAPGLFGTPLLTLSPKVCNFTLASQVPPFSRLDDPAEYHLY 236
 DB 236 GFRTKTVAREVASRINNVAVAPGFISSDMSKLGDDINKRIETIPL-GRYQPEVAVL 294
 QY 237 VQAITENP---PLNGEVIRLDGAI 259
 DB 295 VEFLANPASPSTYTGQVFTIDGGM 320

RESULT 15
 C83961
 3-oxoacyl-(acyl-carrier protein) reductase fabg [imported] - Bacillus halodurans (st
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 03-Aug-2001
 C:Accession: C83961
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.;
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
 A:Reference number: A83650; MIMD:20512582; PMID:11058132
 A:Accession: C83961
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-246 <STO>
 A:Cross-references: GB:AP001515; GB:BA000004; NID:q10174886; PIDN:BAB06210.1; GSPDB:
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: fabg
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.6%; Score 333.5; DB 2; Length 246;
 Best Local Similarity 34.2%; Pred. No. 6.6e-19;
 Matches 90; Conservative 42; Mismatches 102; Indels 29; Gaps 7;

QY 8 VKGLVAVITGGASGLIATAEELVGGASAVLDDLPNSGE-----AQAKRLGNVCV 59
 DB 2 LGKTAIVTASGIGKATAMELARIGANVY---NYAGNKKAEKVAEIKELGVEAI 57
 QY 60 FAPADYSEKDVQALALAKKGRGRVAVNCAGINVASKITKKGQHTLEDQRVLD 119
 DB 58 AIGADVADSESVQAMVETIDTGAVIDILVNNAGITRDNLNEMRKE-----EDWAVYLD 111
 QY 120 VNLGTFNVIRLVAGENGQNEPDQGRV-GVINTASVAFAEGVQQAAYSAKSGIVM 178
 DB 112 TNLKGVHCKKATYRPMK-----QRRRIINSSVYVAGINAGANVYAAKAGVIGL 164
 QY 179 TLPARDLAPICIRVMTIAPGLFGTPLLTLSPKVCNFTLASQVPPFSRLDDPAEYHLY 238
 DB 165 TKTLARLARINNTVNVAVAPGFJETDGTGELPEDVAKQMLGQIPL-ARLQPEVAVAKAV 223
 QY 239 AILEN---PLNGEVIRLDGAI 259
 DB 224 FLASDDASITLGTIIHYNGGM 246

RESULT 16
3-oxoacyl-[acyl-carrier protein] reductase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AH2042
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguen, R.; Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium *Anabaena*
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH2042
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-251 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA073593.1; PID:917130984; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: fabG
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.6%; Score 333.5; DB 2; Length 251;
Best Local Similarity 33.1%; Pred. No. 6,8e-19;
Matches 91; Conservative 46; Mismatches 97; Indels 41; Gaps 7;

QY 1 MAAYRSVKGVAVITGGAGSGIGLTAERLVGGASAVL-----VLLDLPNSGG 47
DB 1 MLILSENLEGGVAVVIGASRGIGRAILELANYGATVYVNVASSSTADEVVAETTGAG 60
QY 48 EAQAKKLGNNCFAPADVTSEEDVOTALALAKGKGRVAVNACAGIYASKTYNLKKQ 107
DB 61 EAVALK-----ADVAGVQVONLNGAIDKFRKIDILVNNAGITFDLTLLRMKP-- 109
QY 108 THTLEDFORLVNLMGTFTNVRILVAGEGQNEPPOGGGQRYITNTASVAAEFGVGA 167
DB 110 ---EDWQAVIDLNTGFLCTRAVSKMLKKO-----RSGKITVITSVAGMGMPGQAN 159
QY 168 YSASKGGIVGMLPIARDLAPIGIRVMTAPGLFPGPLTSLPEKVCNFLASQVPPSRL 227
DB 160 YSAAKAGVIGFTKTVAKELASRGITVNAVAPGFIATDMSTNKSE---GIIGYIPL-GRY 215

QY 228 GDPAEYAHLYQALITENP---FLNGEYIRLDGAIIM 259
DB 216 GQPEETAGMVRFLADPAAPAAVITGOYFVNDGGMMV 250

RESULT 17
3-oxoacyl-[acyl-carrier protein] reductase BH3896 [imported] - *Bacillus halodurans* (strain H84136)
C:Species: *Bacillus halodurans*
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: H84136
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A:Reference number: AB3650; MUID:20512582; PMID:11058132
A:Accession: H84136
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-246 <STO>
A:Cross-references: GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BA07615.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3896
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.5%; Score 332; DB 2; Length 246;
Best Local Similarity 34.2%; Pred. No. 8,7e-19;
Matches 91; Conservative 40; Mismatches 95; Indels 40; Gaps 8;

RESULT 18
3-oxoacyl-[acyl-carrier-protein] reductase VC2021 [imported] - *Vibrio cholerae* (strain F82128)
C:Species: *Vibrio cholerae*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: F82128
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gajin, M.L.; Dodson, J.
charlson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Selzer, L.
R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: AB2035; MUID:20406833; PMID:10952301
A:Accession: F82128
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-248 <HEL>
A:Cross-references: GB:AE004276; GB:AE003852; NID:9656555; PIDN:AE95169.1; GSPDB:AE
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2021
A:Map position: 1
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.2%; Score 328.5; DB 2; Length 248;
Best Local Similarity 32.0%; Pred. No. 1,6e-18;
Matches 82; Conservative 54; Mismatches 103; Indels 17; Gaps 5;

QY 7 SVKGLAVITGASGLGLATAERLVGGASAVLDDLPNSGGEAOAKKLGNNCFAPADVT 66
DB 6 NLEGVAVLVGASRGIGRAIAELLAEBAKAYIGTATSSGQAISDYLGDKGMALNVT 65
QY 67 SEKDQVOTALAKGKGFEGVDVAVNACAGIYASKTYNLKKGQTHLEDFORLVNLMGTFT 126
DB 66 NPESIEAVLKAITDFEGVDLVNNAIGTRNMLRME-----EEMSDIMENILNISIF 119
QY 127 NVIRLVAGEGQNEPPOGGGQRYITNTASVAAEFGVGAAYASKGGIVGMLPIARDL 186
DB 120 RLKRAVLRGMKK-----RGRITVNSVVGTMGNAQAVYAAKAGVIGFTSMAREV 173
QY 187 APIGIRVMTAPGLFPGPLTSLPEKVCNFLASQVPPSRLGDPAEYAHLYQALITENP-- 244
DB 174 ASRGVAVTVAPAGFIETMTKALNDEORTATLAQVP-AGRLGDPREIASAV-ATLASPEA 231

QY 245 -FLNGEYIRLDGAIIM 259
DB 232 AVITGETLVHNGKMTM 247

RESULT 19
3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) [imported] - *Streptococcus*
C:Species: *Streptococcus pneumoniae*

submitted to GenBank, April 2001
 A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139
 A:Accession: D90481
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1299 <KOR>
 A:Cross-references: GB:AE006641; NID:q13816394; PIDN:AAK43107.1; GSPDB:GN00155
 C:Genetics:
 A:Gene: fabG-9
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 24.3%; Score 317; DB 2; Length 299;
 Best Local Similarity 32.5%; Pred. No. 1.7e-17;
 Matches 83; Conservative 47; Mismatches 107; Indels 18; Gaps 5;

QY 12 VAVITGASGLATAERLVGQASAVLLDLPNSGCG--EAQAKKLGNNCFAPADVTSE 68
 DB 4 VSITGGAKGIGALGYRLGKGYAVVIADVEAGKRYRENHFGEGIDSPFIKTVSSSE 63
 QY 69 KDVOALALAKGPERVAVNACINAVASKTYNKKQOTHTLDFORVLVDNLMGTENV 128
 DB 64 MDVSMVERVYGRYRIDVYNNAGIFSGKSI-----EEOQLDEMRVITETNLGVWLC 118
 QY 129 IRLVAGENGONEPDGGRVYINTASVAFEGVQGAAYSASKGIVGWTLPIDRLAP 188
 DB 119 SKYAVKYMKN-----GGVIVNTASTRAFQSEPTBPYSASKGIIATHTSLAVLSK 171
 QY 169 IGRIMTAPGLFGTPLTSLP-EKVCNPLASQVFFPRRLDPATYATLQALLEN--PF 245
 DB 172 YNIRVVISIPGMIDTSMQVPPRESTLSGLDHGHLTRVRKPEDVASLVTVLVSDDASW 231
 QY 246 INGEVIRLDGAIKMQ 260
 DB 232 ISGVNFTTIDGKMTVK 246

RESULT 23
 A48154
 short-chain alcohol dehydrogenase (EC 1.1.1.-) Ke 6 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A48154
 R:Aziz, N.; Maxwell, M.M.; St. Jacques, B.; Brenner, B.M.
 Mol. Cell. Biol. 13, 1847-1853, 1993
 A:Title: Downregulation of Ke 6, a novel gene encoded within the major histocompatibility complex, is essential for the development of the thymus
 A:Reference number: A48154; M01D:93180832; PMID:8441417
 A:Accession: A48154
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-260 <AZI>
 A:Cross-references: GB:U34072; NID:q1103843
 A:Note: sequence extracted from NCBI backbone (NCBIN:126003, NCBIP:126004)
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 C:Keywords: alcohol metabolism; NAD; oxidoreductase
 F:10-199/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 24.2%; Score 315.5; DB 1; Length 260;
 Best Local Similarity 31.0%; Pred. No. 1.8e-17;
 Matches 85; Conservative 55; Mismatches 105; Indels 29; Gaps 9;

QY 1 MAARVSXGLVAVITGA-SGLGLATAERLVGQASAVLLDLPNSGGAQAKKLGNN-- 56
 DB 1 MASQLR-IRGALALVVGAGSGIGRAISVRLAEGAAYACDDGAAADPTVLLGSPGS 59
 QY 57 -----NCVFPADVTSEKDVOTLALAKGKFGV-VDYAVNACIINAVASKTYNKKGO 107
 DB 60 EDGAPRGKHAAP-QADVSQGPAAARLLEEVQACFSPPVYVSCAGITDEFILHSE-- 116
 QY 108 THTLEDFORVLVDNLMGTENVIRLVAGENGONEPDGGRVYINTASVAFEGVQGA 167
 DB 117 -----EDMDRVIAVNIKOTFLVYQAAGALVSS-----GGGSIINISITIKGNIGGIN 167

QY 168 YSASKGIVGMLPIARDLAPIGIRVMTIAPGLFGTPLTSLPEKVCNPLASQVPPPSRL 227
 DB 168 YASSKAGVIGLTTARLEARRHGRICRNSVLPGLIATPPOKPEKVKDYATMIP--GSM 226
 QY 228 GDPAEYAHLYQ--AIENPFLNGEVIRLDGAIK 259
 DB 227 GDPEDYADVAFALASEDSGYITGASVEVSGGLEM 260

RESULT 24
 T36846
 probable dehydrogenase - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-Jan-2000
 C:Accession: T36846
 R:Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, September 1998
 A:Reference number: Z21615
 A:Accession: T36846
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-260 <OLI>
 A:Cross-references: EMBL:AL031541; PIDN:CAA20822.1; GSPDB:GN00070; SCOEDB:SCI35.33c
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SCI35.33c
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 24.2%; Score 315.5; DB 2; Length 260;
 Best Local Similarity 36.7%; Pred. No. 1.8e-17;
 Matches 95; Conservative 33; Mismatches 110; Indels 21; Gaps 9;

QY 6 RSVKGLAVITGASGLATAERLVGQASAVLLDLPNSGCGEAQAKKLGNNCFAPADY 65
 DB 8 RRLVGRVAVVYAGSSGIGLATRRLASEGAVHVGCDVETGRRAAETGG--TEVQADV 65
 QY 66 TSEKDVOTLALAKGPERVAVNACINAVASKTYNKKQOTHTLDFORVLVDNLMGT 125
 DB 66 TDPEQVEALFPAADVTGSDVAFNNAGISPPDDSTLENG----LEAMRGVEVNLTSV 121
 QY 126 FNVLRLVAGENGONEPDGGRVYINTAS-VAAFEQVQGAAYSASKGIVGWTLPIDAR 184
 DB 122 YLCKKAAPYKRR---QG--RGSIIYNTASVAFAMGATSGISTASKGVLASRELGV 175
 QY 185 DLAPIGIRVMTIAPGLFGTPLTSLP--PEKVCNPLASQVFFPRRLDPATYATLQAL 238
 DB 176 QFARGGIRVNMALCPEDVDTPLRLFAKDPERRARLV-HIPV-CRAFAEETIAAAYAF 233
 QY 239 AIENPFLNGEVIRLDGAI 257
 DB 234 ASDSSFYVATDFLVDGCI 252

RESULT 25
 T11579
 probable short chain alcohol dehydrogenase CPD12, drought-inducible - cowpea
 C:Species: Vigna unguiculata (cowpea)
 C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000
 C:Accession: T11579
 R:Lucchi, S.; Yamauchi-Shinozaki, K.; Urao, T.; Shinozaki, K.
 J. Plant Res. 109, 415-424, 1996
 A:Title: Characterization of two cDNAs for novel drought-inducible genes in the hsp

A:Reference number: T11579
 A:Accession: T11579
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-267 <TUC>
 A:Cross-references: EMBL:D88121
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 24.2%; Score 315; DB 2; Length 267;
 Best Local Similarity 34.1%; Pred. No. 2.1e-17;
 Matches 90; Conservative 45; Mismatches 107; Indels 22; Gaps 6;

Thu Jun 26 06:55:08 2003

us-09-931-186-4.rpr

Page 10

```
OY 1 MAAVRSYKGLVAVITGGASGLATARLVGGSASAVLLDLPNSGGGAOAKKLGNCVF 60
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 LSPVVKRLEKGVAILITGGASGIGETARLFESOHGAHYVADIQDDVGLSLCNEI-KSAIY 65
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 61 APADVTSKDVQOTALALAKGKFGHVDVAVNOCAGIAVASKTYNKKGQTHLEDEORVLDY 120
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 VHCYTKEDIEKCVDTAVSKFGKLDIMFNNAIGDEPK---KSIDNTKSDPERVYSV 121
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 121 NLMGTFNVIRLVAGEMGQNEPDGQGRGVIIINTASVAFEGQVQAAYSASKGGIVGML 180
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 NLVGPFLGTKEAARVM-----IPARRGCIINTASVAGCIGGATHAYTSKHALVGLTK 175
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 181 PIARDLAPIGIRVMTIAPGLEGTPLT---SLPE---KYCNFLASQVPPPSRLGDPAEY 233
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 176 NTAVELGQFGIRVNCVSPFAIVTPLLNKYNLDEEGVRYKTYMNLKGYVPVNDVAEALY 235
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 234 AHLVQAIIEPNPFLNGEVIRLDGAI 257
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 236 L---ASDESKFVSSHNLVIDGGL 255
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: June 23, 2003, 14:34:18
Job time : 17.8333 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 14:32:58 ; Search time 20.333 Seconds

(Without alignments)
1388.950 Million cell updates/sec

Title: US-09-931-186-4

Perfect score: 1304

Sequence: 1 MAAAVRSVKGLVAIVTGAS.....ENPFLNGEYIRLDGARIMQP 261

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications: AA:*
1: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pep:*
2: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
7: /cgn2_6/prodata/1/pubppa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB.pep:*
10: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pep:*
12: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep:*
13: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep:*
14: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1304	100.0	261	10 US-09-931-186-4	Sequence 4, Appl1
2	1299	99.6	261	10 US-09-931-186-8	Sequence 8, Appl1
3	1290	98.9	261	10 US-09-931-186-20	Sequence 20, Appl1
4	1289	98.8	261	10 US-09-931-186-6	Sequence 6, Appl1
5	1289	98.8	261	10 US-09-931-186-23	Sequence 23, Appl1
6	1287	98.7	261	10 US-09-931-186-2	Sequence 2, Appl1
7	1146	87.9	227	9 US-09-984-245-245	Sequence 245, App
8	1146	87.9	227	9 US-09-966-262-245	Sequence 245, App
9	1146	87.9	227	9 US-09-963-966-245	Sequence 245, App
10	1146	87.9	227	9 US-10-143-090-245	Sequence 245, App
11	664.5	51.0	388	9 US-09-920-923-41	Sequence 41, Appl
12	332.5	25.5	259	10 US-09-931-186-17	Sequence 17, Appl
13	332.5	25.5	243	10 US-09-815-242-13360	Sequence 13360, A
14	326.5	25.0	243	10 US-09-815-242-13581	Sequence 13581, A
15	318.5	24.4	243	10 US-09-815-242-10921	Sequence 10921, A
16	314	24.1	237	9 US-10-175-696-14	Sequence 14, Appl
17	314	24.1	237	10 US-09-823-901-2	Sequence 2, Appl1
18	305.5	23.4	253	10 US-09-931-186-15	Sequence 15, Appl1
19	301	23.1	247	9 US-09-479-040-9	Sequence 9, Appl1

20	293.5	22.5	267	9 US-09-773-748-1	Sequence 1, Appl1
21	292.5	22.4	262	9 US-10-307-385-6	Sequence 6, Appl1
22	292.5	22.4	262	10 US-09-802-553-6	Sequence 6, Appl1
23	291.5	22.4	270	9 US-09-978-255A-468	Sequence 468, App
24	291.5	22.4	270	9 US-09-978-657-468	Sequence 468, App
25	291.5	22.4	270	9 US-09-978-192A-468	Sequence 468, App
26	291.5	22.4	270	9 US-09-999-832A-468	Sequence 468, App
27	291.5	22.4	270	9 US-09-978-189-468	Sequence 468, App
28	291.5	22.4	270	9 US-09-978-608A-468	Sequence 468, App
29	291.5	22.4	270	9 US-09-981-915A-468	Sequence 468, App
30	291.5	22.4	270	9 US-09-999-833A-468	Sequence 468, App
31	291.5	22.4	270	9 US-10-167-749-468	Sequence 468, App
32	291.5	22.4	270	9 US-09-978-403A-468	Sequence 468, App
33	291.5	22.4	270	9 US-09-978-564A-468	Sequence 468, App
34	291.5	22.4	270	9 US-09-978-585A-468	Sequence 468, App
35	291.5	22.4	270	9 US-10-017-081A-468	Sequence 468, App
36	291.5	22.4	270	9 US-09-978-824-468	Sequence 468, App
37	291.5	22.4	270	9 US-09-981-915A-468	Sequence 468, App
38	291.5	22.4	270	9 US-09-999-833A-468	Sequence 468, App
39	291.5	22.4	270	9 US-10-167-749-468	Sequence 468, App
40	291.5	22.4	270	9 US-09-978-403A-468	Sequence 468, App
41	291.5	22.4	270	9 US-09-978-564A-468	Sequence 468, App
42	291.5	22.4	270	9 US-09-978-585A-468	Sequence 468, App
43	291.5	22.4	270	9 US-10-017-081A-468	Sequence 468, App
44	291.5	22.4	270	9 US-09-978-824-468	Sequence 468, App
45	291.5	22.4	270	9 US-09-981-915A-468	Sequence 468, App
46	291.5	22.4	270	9 US-09-999-833A-468	Sequence 468, App
47	291.5	22.4	270	9 US-10-167-749-468	Sequence 468, App
48	291.5	22.4	270	9 US-09-978-403A-468	Sequence 468, App
49	289.5	22.2	244	10 US-09-815-242-10126	Sequence 10126, A
50	288.5	22.1	642	9 US-09-364-847-59	Sequence 59, Appl
51	288	22.1	263	10 US-09-815-242-14092	Sequence 14092, A
52	288	22.1	641	9 US-09-364-847-10	Sequence 10, Appl
53	287.5	22.0	246	9 US-09-364-847-6	Sequence 6, Appl
54	287.5	22.0	641	9 US-09-364-847-19	Sequence 19, Appl
55	287.5	22.0	642	9 US-09-364-847-61	Sequence 61, Appl
56	285.5	21.9	244	9 US-09-849-092-13	Sequence 13, Appl
57	283.5	21.7	203	9 US-10-175-656-19	Sequence 19, Appl
58	283.5	21.7	203	10 US-09-823-901-7	Sequence 7, Appl1
59	276	21.2	258	9 US-09-738-626-636	Sequence 636, App
60	276	21.2	285	10 US-09-815-242-10241	Sequence 10241, A
61	274.5	21.1	254	9 US-09-978-758-2	Sequence 2, Appl1
62	274	21.0	206	9 US-09-978-816-4	Sequence 4, Appl1
63	273.5	21.0	272	10 US-09-815-242-12688	Sequence 12688, A
64	272.5	20.9	286	10 US-09-815-242-11860	Sequence 11860, A
65	271.5	20.8	251	10 US-09-815-242-5689	Sequence 5689, App
66	269.5	20.7	246	10 US-09-815-242-9461	Sequence 9461, App
67	269.5	20.7	246	10 US-09-815-242-12123	Sequence 12123, A
68	269.5	20.7	246	10 US-09-815-242-12803	Sequence 12803, A
69	269.5	20.7	246	10 US-09-815-242-13100	Sequence 13100, A
70	268	20.6	251	9 US-10-272-419-20	Sequence 20, Appl
71	266.5	20.4	242	10 US-09-815-242-10974	Sequence 10974, A
72	266	20.4	256	10 US-09-954-314-14	Sequence 14, Appl
73	264	20.2	276	9 US-09-944-160-24	Sequence 24, Appl
74	262.5	20.1	252	9 US-09-910-033A-2	Sequence 2, Appl1
75	262.5	20.1	258	9 US-10-156-055A-1	Sequence 1, Appl1
76	259	19.9	263	10 US-09-815-242-11842	Sequence 11842, A
77	257	19.7	261	9 US-09-971-536-74	Sequence 74, Appl1
78	254	19.5	261	10 US-09-940-037A-29	Sequence 29, Appl
79	250.5	19.2	266	9 US-09-981-353-40	Sequence 40, Appl
80	250.5	19.2	266	9 US-09-885-303A-22	Sequence 22, Appl
81	250.5	19.2	266	9 US-10-205-823-176	Sequence 176, App
82	250.5	19.2	266	10 US-09-931-186-18	Sequence 18, Appl
83	250	19.2	262	10 US-09-764-853-553	Sequence 553, App
84	245.5	18.8	262	10 US-09-815-242-10597	Sequence 10597, A
85	242.5	18.6	261	10 US-09-815-242-10846	Sequence 10846, A
86	241	18.5	251	10 US-09-923-501-16	Sequence 16, Appl
87	239	18.3	255	10 US-09-931-186-14	Sequence 14, Appl
88	238	18.3	247	10 US-09-815-242-11893	Sequence 11893, A
89	238	18.3	258	10 US-09-954-314-12	Sequence 12, Appl
90	237.5	18.2	274	9 US-09-976-059-17	Sequence 17, Appl
91	235	18.0	271	10 US-09-815-242-13387	Sequence 13387, A
92	235	18.0	272	10 US-09-815-242-13679	Sequence 13679, A

```

93      233      17.9      311      9      US-09-738-626-3819      Sequence 3819, Ap
94      232      17.8      261      10      US-09-815-242-5813      Sequence 5813, Ap
95      225.5      17.3      247      10      US-09-815-242-11342      Sequence 11342, A
96      224      17.2      254      10      US-09-741-669-411      Sequence 411, App
97      232.5      17.1      247      10      US-09-815-242-11514      Sequence 11514, A
98      222.5      17.1      900      9      US-10-060-230-15      Sequence 15, Appl
99      222.5      17.1      900      9      US-10-060-230-17      Sequence 17, Appl
100     216.5      16.6      253      10      US-09-815-242-10279      Sequence 10279, A

```

ALIGNMENTS

```

RESULT 1
US-09-931-186-4      Application US/09931186
; Sequence 4, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: AGRE, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOMALTER, RICHARD E.
; APPLICANT: TEMPCEZYK-RUSSELL, ANNA
; APPLICANT: THOMSON, JIM
; APPLICANT: VANDERPOOL, DARIN
; APPLICANT: VILLAFRANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931,186
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 261
; TYPE: PR
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: full length mutant ERAB CSV
US-09-931-186-4
Query Match      100.0%; Score 1304; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.1e-110;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1      MAAVRSYKGLVAVITGASGLGATAEKLVGOGASAVLLDLPNSGGEQAOKKLNCCVF 60
DB      1      MAAVRSYKGLVAVITGASGLGATAEKLVGOGASAVLLDLPNSGGEQAOKKLNCCVF 60
QY      61      APADVTSEKDVOTATLAKGKFRGVDAVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120
DB      61      APADVTSEKDVOTATLAKGKFRGVDAVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120
QY      121     NMGTENVIRLVAGEMGNEPDGGRGVIIINTASVAAFEGOVGOAAYSASKGGIVGML 180
DB      121     NMGTENVIRLVAGEMGNEPDGGRGVIIINTASVAAFEGOVGOAAYSASKGGIVGML 180
QY      181     PIARDLAPIGIRMTIAPGLFGTPLLTSLEPKVCNFIASQVFPFSLGDPATYAHLYQAI 240
DB      181     PIARDLAPIGIRMTIAPGLFGTPLLTSLEPKVCNFIASQVFPFSLGDPATYAHLYQAI 240
QY      241     IENPFLNGEVIIRLDGAIRMOP 261
DB      241     IENPFLNGEVIIRLDGAIRMOP 261
RESULT 2

```

```

US-09-931-186-8
; Sequence 8, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: AGRE, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOMALTER, RICHARD E.
; APPLICANT: TEMPCEZYK-RUSSELL, ANNA
; APPLICANT: THOMSON, JIM
; APPLICANT: VANDERPOOL, DARIN
; APPLICANT: VILLAFRANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931,186
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 8
; LENGTH: 261
; TYPE: PR
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: wild type ERAB
US-09-931-186-8
Query Match      99.6%; Score 1299; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 8.9e-110;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1      MAAVRSYKGLVAVITGASGLGATAEKLVGOGASAVLLDLPNSGGEQAOKKLNCCVF 60
DB      1      MAAVRSYKGLVAVITGASGLGATAEKLVGOGASAVLLDLPNSGGEQAOKKLNCCVF 60
QY      61      APADVTSEKDVOTATLAKGKFRGVDAVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120
DB      61      APADVTSEKDVOTATLAKGKFRGVDAVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120
QY      121     NMGTENVIRLVAGEMGNEPDGGRGVIIINTASVAAFEGOVGOAAYSASKGGIVGML 180
DB      121     NMGTENVIRLVAGEMGNEPDGGRGVIIINTASVAAFEGOVGOAAYSASKGGIVGML 180
QY      181     PIARDLAPIGIRMTIAPGLFGTPLLTSLEPKVCNFIASQVFPFSLGDPATYAHLYQAI 240
DB      181     PIARDLAPIGIRMTIAPGLFGTPLLTSLEPKVCNFIASQVFPFSLGDPATYAHLYQAI 240
QY      241     IENPFLNGEVIIRLDGAIRMOP 261
DB      241     IENPFLNGEVIIRLDGAIRMOP 261
RESULT 3
US-09-931-186-20
; Sequence 20, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: AGRE, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOMALTER, RICHARD E.
; APPLICANT: TEMPCEZYK-RUSSELL, ANNA

```